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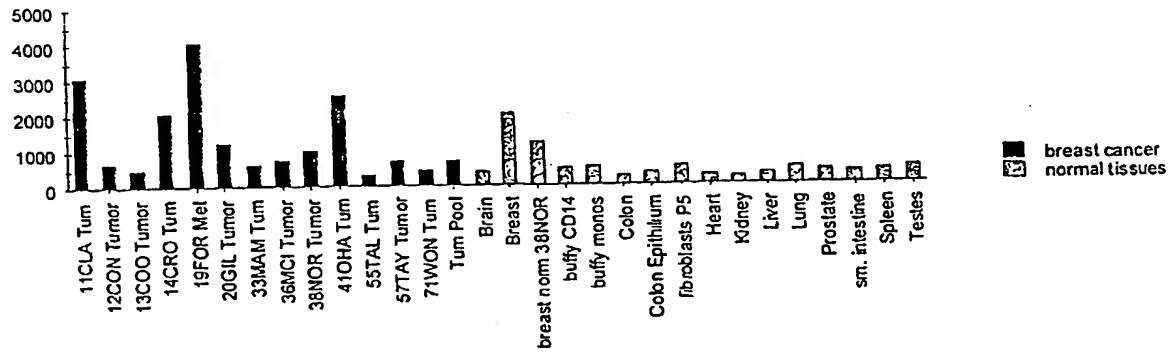

(57) Abstract

Described herein are methods that can be used for diagnosis and prognosis of breast cancer. Also described herein are methods that can be used to screen candidate bioactive agents for the ability to modulate breast cancer. Additionally, methods and molecular targets (genes and their products) for therapeutic intervention in breast and other cancers are described.

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NOVEL METHODS OF DIAGNOSING AND TREATING BREAST CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR BREAST CANCER MODULATORS

FIELD OF THE INVENTION

The invention relates to the identification of expression profiles and the nucleic acids involved in breast cancer, and to the use of such expression profiles and nucleic acids in diagnosis, prognosis and treatment of breast cancer. The invention further relates to methods for identifying and using candidate agents and/or targets which modulate breast cancer.

BACKGROUND OF THE INVENTION

Breast cancer is a significant cancer in Western populations. It develops as the result of a pathologic transformation of normal breast epithelium to an invasive cancer. There have been a number of recently characterized genetic alterations that have been implicated in breast cancer. However, there is a need to identify all of the genetic alterations involved in the development of breast cancer.

Imaging of breast cancer for diagnosis has been problematic and limited. In addition, dissemination of tumor cells (metastases) to locoregional lymph nodes is an important prognostic factor; five year survival rates drop from 80 percent in patients with no lymph node metastases to 45 to 50 percent in those patients who do have lymph node metastases. A recent report showed that micrometastases can be detected from lymph nodes using reverse transcriptase-PCR methods based on the presence of mRNA for carcinoembryonic antigen, which has previously been shown to be present in the vast majority of breast cancers but not in normal tissues. Liefers et al., New England J. of Med. 339(4):223 (1998).

Thus, methods that can be used for diagnosis and prognosis of breast cancer would be desirable. While academia and industry has made an effort to identify novel sequences, there has not been an equal effort exerted to identify the function of the novel sequences. For example, databases show the

sequence of accession number W72838, but there no data correlating this sequence with a function, much less a disease state. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of breast cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate breast cancer. Additionally, provided herein are molecular targets for therapeutic intervention in breast and other cancers.

SUMMARY OF THE INVENTION

The present invention provides methods for screening for compositions which modulate breast cancer. Also provided herein are methods of inhibiting proliferation of a cell, preferably a breast cancer cell. Methods of treatment of cancer, as well as compositions, are also provided herein.

In one aspect, a method of screening drug candidates comprises providing a cell that expresses an expression profile gene or fragments thereof. Preferred embodiments of the expression profile gene are genes which are differentially expressed in cancer cells, preferably breast cancer cells, compared to other cells. Preferred embodiments of expression profile genes used in the methods herein include but are not limited to the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2; fragments of the proteins of this group are also preferred. In another embodiment, a nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided herein is a method of screening for a bioactive agent capable of binding to a breast cancer modulator protein (BCMP), the method comprising combining the BCMP and a candidate bioactive agent, and determining the binding of the candidate agent to the BCMP. Preferably the BCMP is a protein or fragment thereof selected from the group consisting of BCR3, BCQ8, BCQ5,

BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12.

Further provided herein is a method for screening for a bioactive agent capable of modulating the activity of a BCMP. In one embodiment, the method comprises combining the BCMP and a candidate bioactive agent, and determining the effect of the candidate agent on the bioactivity of the BCMP. Preferably the BCMP is a protein or fragment thereof selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12.

Also provided is a method of evaluating the effect of a candidate breast cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the BCMP, or an animal lacking the BCMP, for example as a result of a gene knockout.

Additionally, provided herein is a method of evaluating the effect of a candidate breast cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual.

Moreover, provided herein is a biochip comprising a nucleic acid segment which encodes a breast cancer protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2, or a fragment thereof, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably at least two nucleic acid segments are included. In another embodiment, the nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12.

Furthermore, a method of diagnosing a disorder associated with breast cancer is provided. The method comprises determining the expression of a gene which encodes a breast cancer protein preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5,

BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2 or a fragment thereof in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12. A difference in the expression indicates that the first individual has a disorder associated with breast cancer.

In another aspect, the present invention provides an antibody which specifically binds to a breast cancer protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12. In a preferred embodiment, the fragment of BCH1 is selected from BCH1p1 and BCH1p2. Other preferred fragments for the breast cancer proteins are shown in the figures. Preferably the antibody is a monoclonal antibody. The antibody can be a fragment of an antibody such as a single stranded antibody as further described herein, or can be conjugated to another molecule. In one embodiment, the antibody is a humanized antibody.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a breast cancer protein (BCMP) or a fragment thereof and an antibody which binds to said BCMP or fragment thereof. In a preferred embodiment, the method comprises combining a BCMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said BCMP or fragment thereof. The method further includes determining the binding of said BCMP or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the antibody as well as the agent inhibits breast cancer.

In a further aspect, a method for inhibiting breast cancer is provided. In one embodiment, the method comprises administering to a cell a composition comprising an antibody to a breast modulating protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12.

The method can be performed in vitro or in vivo, preferably in vivo to an individual. In a preferred embodiment the method of inhibiting breast cancer is provided to an individual with cancer. As described herein, methods of inhibiting breast cancer can be performed by administering an inhibitor of breast cancer protein activity, including an antisense molecules, and preferably small molecules.

Also provided herein are methods eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising a breast modulating protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12. In another aspect, said composition comprises a nucleic acid comprising a sequence encoding a breast modulating protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2, or a fragment thereof. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a breast modulating protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a breast modulating protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12.

A method of neutralizing the effect of a breast cancer protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2, or a fragment thereof, is also provided. Preferably, the method comprises

contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12.

In another aspect of the invention, a method of treating an individual for breast cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of BCH1. In another embodiment, the individual is non-responsive to an anti-estrogen and is positive for estrogen receptor. Optionally, the method further comprises administering an anti-estrogen to said individual.

Also provided herein is method for determining the prognosis of an individual with breast cancer comprising determining the level of BCH1 in a sample, wherein a high level of BCH1 indicates a poor prognosis. Moreover, in yet another aspect of the invention, a method is provided for determining whether an individual with breast cancer will be non-responsive to anti-estrogen therapies comprising determining the level of BCH1 wherein a high level of BCH1 indicates that an individual will be non-responsive. Preferably, the methods herein are used to identify persons who are tamoxifen resistant.

Novel sequences are also provided herein. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

DETAILED DESCRIPTION OF THE FIGURES

Figure 1 provides the Accession numbers for genes, including expression sequence tags, (incorporated in their entirety here and throughout the application where Accession numbers are provided), downregulated in tumor tissue compared to normal breast tissue.

Figure 2 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal breast tissue.

Figure 3 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal breast tissue.

Figure 4 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue.

Figure 5 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue.

Figure 6 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue.

Figure 7 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 8 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue. Specifically, one column shows the ratio of expression of the indicated gene in breast tumor tissue compared to other body tissues, and another column shows the ratio of expression of the indicated gene in breast tumor tissue compared to normal breast tissue.

Figure 9 depicts the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue.

Figure 10 depicts a preferred group of 1007 Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue.

Figure 11 depicts a preferred group of 123 Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue.

Figure 12 depicts a preferred group of 10 Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue.

Figure 13 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCR3. The start and stop codons are underlined.

Figure 14 shows an embodiment of an open reading frame of a nucleic acid encoding BCR3, wherein the start and stop codons are underlined.

Figure 15 shows an embodiment of an amino acid sequence of BCR3. The signal peptide is underlined and the transmembrane domain is shaded. In a preferred embodiment, a soluble form of BCR3 is provided wherein the signal peptide is deleted or preferably naturally cleaved, and the transmembrane domain is deleted, inactivated, or BCR3 is truncated to exclude the transmembrane domain.

Figure 16 shows the amino acid sequence of BCR3p1 and BCR3p2.

Figure 17 shows the relative amount of expression of BCR3 in various samples of breast cancer tissue (dark bars) and many normal tissue types (light bars).

Figure 18 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCQ8. The start and stop codon are underlined.

Figure 19 shows an embodiment of an open reading frame of a nucleic acid encoding BCQ8, wherein the start and stop codons are underlined.

Figure 20 shows an embodiment of an amino acid sequence of BCQ8. The signal peptide is underlined twice and the transmembrane domain is underlined. In a preferred embodiment, a soluble form of BCQ8 is provided wherein the signal peptide is deleted, and the transmembrane domain is deleted, inactivated, or BCQ8 is truncated on either end as desired, to exclude the transmembrane domain.

Figure 21 shows the amino acid sequence of BCQ8p1 and BCQ8p2.

Figure 22 shows the relative amount of expression of BCQ8 in various samples of breast cancer tissue (dark bars) and many normal tissue types (light bars).

Figure 23 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a differentially expressed protein provided herein, human BCQ5.

Figure 24 shows an embodiment of an open reading frame of a nucleic acid encoding human BCQ5.

Figure 25 shows embodiments of amino acid sequences of BCQ5 by providing an alignment wherein human is above mouse which is above rat.

Figure 26 shows the amino acid sequence of BCQ5p1, BCQ5p2 and BCQ5p3.

Figure 27 shows the relative amount of expression of BCQ5 in various samples of breast cancer tissue, colorectal cancer tissue, angiogenesis models wherein tubes are formed from endothelial cells, and normal tissue types.

Figure 28 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a differentially expressed protein provided herein, mouse BCQ5.

Figure 29 shows an embodiment of an open reading frame of a nucleic acid encoding mouse BCQ5.

Figure 30 shows an embodiment of a nucleic acid (partial mRNA) which includes a sequence which encodes a differentially expressed protein provided herein, rat BCQ5.

Figure 31 shows an embodiment of a partial open reading frame of a nucleic acid encoding rat BCQ5.

Figure 32 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCH1. Start and stop codons are underlined.

Figure 33 shows an embodiment of an open reading frame of a nucleic acid encoding BCH1, wherein start and stop codons are underlined.

Figure 34 shows an embodiment of an amino acid sequence of BCH1. In a preferred embodiment, isolated BCH1 excludes the signal sequence, amino acids 1-19.

Figure 35 shows the amino acid sequence of BCH1p1 and BCH1p2 (below).

Figure 36 shows the relative amount of expression of BCH1 in various samples of breast cancer tissue (dark bars) and many normal tissue types (light bars).

Figure 37 shows a graph correlating expression of estrogen receptor (ER) (vertical bar) and BCH1 (horizontal bar) with localization to the nucleus (diamonds) or the cytoplasm (squares).

Figures 38A and 38B show breast carcinoma tissue specimens having high levels of BCH1 expression as indicated by anti-BCH1 antibodies.

Figures 39A and 39B show samples taken from the tissues shown in Figures 38A and 38B respectively, wherein anti-estrogen receptor antibodies indicate that estrogen receptor is localized exclusively to the cytoplasm.

Figures 40A and 40B show breast carcinoma tissue specimens having low levels of BCH1 expression as indicated by anti-BCH1 antibodies.

Figures 41A and 41B show samples taken from the tissues shown in Figures 40A and 40B respectively, wherein anti-estrogen receptor antibodies indicate that estrogen receptor in low BCH1 expression tissue does not correlate with estrogen receptor localization.

Figure 42 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCN1. Start and stop codons are shaded, and Accession number AA419622 sequence is underlined.

Figure 43 shows an embodiment of an amino acid sequence of BCN1. A putative transmembrane domain is predicted to be at least at approximately positions 201-217 and 67-83. The protein may be a type IIIa membrane protein and may have additional transmembrane domains.

Figure 44 shows the amino acid sequence of BCN1p1 and BCN1p2.

Figure 45 shows the relative amount of expression of BCN1 in various samples of breast cancer tissue (dark bars), colon cancer tissue (light bars) and many normal tissue types (medium light dotted bars).

Figures 46A-46D show an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCN2. Start and stop codons are shaded, and Accession number AA428090 sequence is underlined.

Figure 47 shows an embodiment of an amino acid sequence of BCN2.

Figure 48 shows the relative amount of expression of BCN2 in various samples of breast cancer tissue (dark bars), colon cancer tissue (light bars) and many normal tissue types (medium light dotted bars).

Figures 49A-49B show an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCN5. Start and stop codons are shaded, and Accession number R51309 sequence is underlined.

Figure 50 shows an embodiment of an amino acid sequence of BCN5. A putative signal sequence is shaded and preferred sequence is underlined.

Figure 51 shows the relative amount of expression of BCN5 in various samples of breast cancer tissue (dark bars), colon cancer tissue (light bars) and many normal tissue types (medium light dotted bars).

Figure 52 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCO2. Start and stop codons are underlined.

Figure 53 shows an embodiment of an open reading frame of a nucleic acid encoding BCO2.

Figure 54 shows an embodiment of an amino acid sequence of BCO2.

Figure 55 shows an alignment of amino acids for human BCO2 above mouse BCO2.

Figure 56 shows the relative amount of expression of BCO2 in various samples of breast cancer tissue (dark bars) and many normal tissue types (light bars).

Figure 57 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCX2. Start and stop codons are underlined.

Figure 58 shows an embodiment of an open reading frame of a nucleic acid encoding BCX2.

Figure 59 shows an embodiment of an amino acid sequence of BCX2.

Figure 60 shows the relative amount of expression of BCX2 in various samples of breast cancer tissue (dark bars) and many normal tissue types (light bars).

Figure 61 shows the relative amount of expression of BCX2 in various samples of colon cancer tissue (light bars), non-cancer cell lines (dark bars) and many cell lines (medium light bars).

Figure 62 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCX3. Start and stop codons are underlined.

Figure 63 shows an embodiment of an open reading frame of a nucleic acid encoding BCX3.

Figure 64 shows an embodiment of an amino acid sequence of BCX3.

Figure 65 shows the relative amount of expression of BCX3 in various samples of breast cancer tissue (dark bars) and many normal tissue types (light bars).

Figure 66 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCA2. Start and stop codons are shaded, and Accession number D12485 sequence is underlined.

Figure 67 shows an embodiment of an amino acid sequence of BCA2.

Figure 68 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCR2. Start and stop codons are shaded, and Accession number AA609773 sequence is shown underlined.

Figure 69 shows an embodiment of an amino acid sequence of BCR2.

Figure 70 shows the relative amount of expression of BCR2 in various samples of breast cancer tissue.

Figure 71 shows the relative amount of expression of BCR2 in various samples of normal tissue types (light bars).

Figure 72 shows an embodiment of a nucleic acid which includes a sequence which encodes a breast cancer protein provided herein, BCJ7.

Figure 73 shows an embodiment of a nucleic acid which includes a sequence which encodes a breast cancer protein provided herein, BCY3.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides novel methods for diagnosis and prognosis evaluation for breast cancer, as well as methods for screening for compositions which modulate breast cancer. In one aspect, the expression levels of genes are determined in different patient samples for which either diagnosis or prognosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. That is, normal tissue may be distinguished from breast cancer tissue, and within breast cancer tissue, different prognosis states (good or poor long term survival prospects, for example) may be determined. By comparing expression profiles of breast tissue in known different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. The identification of sequences that are differentially expressed in breast cancer versus normal breast tissue, as well as differential expression resulting in different prognostic outcomes, allows the use of this information in a number of ways. For example, the evaluation of a particular treatment regime may be evaluated: does a chemotherapeutic drug act to improve the long-term prognosis in a particular patient. Similarly, diagnosis may be done or confirmed by comparing patient samples with the known expression profiles. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; for example, screening can be done for drugs that suppress the breast cancer expression profile or convert a poor prognosis profile to a better prognosis profile. This may be done by making biochips comprising sets of the important breast cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the breast cancer proteins can be evaluated for diagnostic and prognostic purposes or to screen candidate agents. In addition, the breast cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the breast cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in breast cancer, breast cancer, herein termed "breast cancer sequences". As outlined below, breast cancer sequences include those that are up-regulated (i.e. expressed at a higher level) in breast cancer, as well as those that are down-regulated (i.e. expressed at a lower level) in breast cancer. In a preferred embodiment, the breast cancer sequences are from humans; however, as will be appreciated by those in the art, breast cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other breast cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc). Breast cancer sequences from other organisms may be obtained using the techniques outlined below.

Breast cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the breast cancer sequences are recombinant nucleic acids. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid by polymerases and endonucleases, in a form not normally found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e. using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e. through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a breast cancer protein from one organism in a

different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

In a preferred embodiment, the breast cancer sequences are nucleic acids. As will be appreciated by those in the art and is more fully outlined below, breast cancer sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; for example, biochips comprising nucleic acid probes to the breast cancer sequences can be generated. In the broadest sense, then, by "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate (Beaucage et al., Tetrahedron 49(10):1925 (1993) and references therein; Letsinger, J. Org. Chem. 35:3800 (1970); Sprinzl et al., Eur. J. Biochem. 81:579 (1977); Letsinger et al., Nucl. Acids Res. 14:3487 (1986); Sawai et al, Chem. Lett. 805 (1984), Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); and Pauwels et al., Chemica Scripta 26:141 91986)), phosphorothioate (Mag et al., Nucleic Acids Res. 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., J. Am. Chem. Soc. 111:2321 (1989), O-methylphophoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, J. Am. Chem. Soc. 114:1895 (1992); Meier et al., Chem. Int. Ed. Engl. 31:1008 (1992); Nielsen, Nature, 365:566 (1993); Carlsson et al., Nature 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., Proc. Natl. Acad. Sci. USA 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi et al., Angew. Chem. Intl. Ed. English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medicinal Chem. Lett. 4:395 (1994); Jeffs et al., J. Biomolecular NMR 34:17 (1994); Tetrahedron Lett. 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also

included within one definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done for a variety of reasons, for example to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip.

As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (Tm) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in Tm for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand ("Watson") also defines the sequence of the other strand ("Crick"); thus the sequences described herein also includes the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A breast cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the breast cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

The breast cancer sequences of the invention can be identified as follows. Samples of normal and tumor tissue are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is know in the art for the preparation of mRNA. Suitable biochips are commercially available, for example from Affymetrix. Gene expression profiles as described herein are generated, and the data analyzed.

In a preferred embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, but not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and placenta. In a preferred embodiment, those genes identified during the breast cancer screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, breast cancer sequences are those that are up-regulated in breast cancer; that is, the expression of these genes is higher in breast carcinoma as compared to normal breast tissue. "Up-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al., Nucleic Acids Research 26:1-7 (1998) and http://www.ncbi.nlm.nih.gov/. In addition, these genes were found to be expressed in a limited relative amount or not at all in heart, brain, lung, liver, kidney, prostate, small intestine, testes, fibroblasts and spleen.

In a preferred embodiment, breast cancer sequences are those that are down-regulated in breast cancer; that is, the expression of these genes is lower in breast carcinoma as compared to normal breast tissue. "Down-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Breast cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In a preferred embodiment the breast cancer protein is an intracellular protein. Intracellular proteins are involved in all aspects of cellular function and replication (including, for example, signaling pathways); aberrant expression of such proteins results in unregulated or disregulated cellular processes. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing intracellular proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

In a preferred embodiment, the breast cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span the phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Important transmembrane protein receptors include, but are not limited to insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL-1 receptor, IL-2 receptor, etc.

Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions. It is understood that the transmembrane domains may be removed to create soluble proteins herein.

Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell for example via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Breast cancer proteins that are transmembrane are particularly preferred in the present invention as they are good targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities.

In a preferred embodiment, the breast cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway.. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. Breast cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, for example for blood tests.

A breast cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology to the breast cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

As used herein, a nucleic acid is a "breast cancer nucleic acid" if the overall homology of the nucleic acid sequence to the nucleic acid sequences encoding the amino acid sequences of the figures is preferably greater than about 75%, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. Homology in this context means sequence similarity or identity, with identity being preferred. A preferred comparison for homology purposes is to compare the sequence containing sequencing errors to the correct sequence. This homology will be determined using standard techniques known in the art, including, but not limited to, the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biool. 48:443 (1970), by the search for similarity method of Pearson & Lipman, PNAS USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, WI), the Best Fit sequence program described by

Devereux et al., Nucl. Acid Res. 12:387-395 (1984), preferably using the default settings, or by inspection.

In a preferred embodiment, the sequences which are used to determine sequence identity or similarity are selected from the sequences set forth in the figures. In one embodiment the sequences utilized herein are those set forth in the figures. In another embodiment, the sequences are naturally occurring allelic variants of the sequences set forth in the figures. In another embodiment, the sequences are sequence variants as further described herein.

One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, J. Mol. Evol. 35:351-360 (1987); the method is similar to that described by Higgins & Sharp CABIOS 5:151-153 (1989). Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

Another example of a useful algorithm is the BLAST algorithm, described in Altschul et al., J. Mol. Biol. 215, 403-410, (1990) and Karlin et al., PNAS USA 90:5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul et al., Methods in Enzymology, 266: 460-480 (1996); http://blast.wustl/edu/blast/ README.html]. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span =1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "longer" sequence in the aligned region. The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).

Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues of the se. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

The alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleosides than those of the figures, it is understood that the percentage of homology will be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, for example, homology of sequences shorter than those of the sequences identified herein and as discussed below, will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, for example, nucleic acids which hybridize under high stringency to the nucleic acid sequences which encode the proteins identified in the figures, or their complements, are considered a breast cancer sequence. High stringency conditions are known in the art; see for example Maniatis et al., Molecular Cloning: A Laboratory Manual, 2d Edition, 1989, and Short Protocols in Molecular Biology, ed. Ausubel, et al., both of which are hereby incorporated by reference. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength pH. The Tm is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at Tm, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g. 10 to 50 nucleotides) and at least about 60°C for long probes (e.g. greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

In another embodiment, less stringent hybridization conditions are used; for example, moderate or low stringency conditions may be used, as are known in the art; see Maniatis and Ausubel, supra, and Tijssen, supra.

In addition, the breast cancer nucleic acid sequences of the invention are fragments of larger genes, i.e. they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding

regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, additional sequences of the breast cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Maniatis et al., and Ausubel, et al., supra, hereby expressly incorporated by reference.

Once the breast cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire breast cancer nucleic acid. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant breast cancer nucleic acid can be further-used as a probe to identify and isolate other breast cancer nucleic acids, for example additional coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant breast cancer nucleic acids and proteins.

The breast cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the breast cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, for example for gene therapy and/or antisense applications. Alternatively, the breast cancer nucleic acids that include coding regions of breast cancer proteins can be put into expression vectors for the expression of breast cancer proteins, again either for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to breast cancer nucleic acids (both the nucleic acid sequences encoding peptides outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the breast cancer nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e. have some sequence in common), or separate.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of either electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of

possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluorescese. A preferred substrate is described in copending application entitled A Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, for example, the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, for example using linkers as are known in the art; for example, homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, the oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In an additional embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

In a preferred embodiment, breast cancer nucleic acids encoding breast cancer proteins are used to make a variety of expression vectors to express breast cancer proteins which can then be used in screening assays, as described below. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the breast cancer protein. The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. The transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the breast cancer protein; for example, transcriptional and translational regulatory nucleic acid sequences from *Bacillus* are preferably used to express the breast cancer protein in *Bacillus*. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, the transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, the expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The breast cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a breast cancer protein, under the appropriate conditions to induce or cause expression of the breast cancer protein. The conditions appropriate for breast cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Drosophila melangaster* cells, *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, THP1 cell line (a macrophage cell line) and human cells and cell lines.

In a preferred embodiment, the breast cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral systems. A preferred expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenlytion signals include those derived form SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, breast cancer proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; for example, the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the breast cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that

have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, breast cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, breast cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillerimondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The breast cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, for example, for the creation of monoclonal antibodies, if the desired epitope is small, the breast cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the breast cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the breast cancer protein is a breast cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In one embodiment, the breast cancer nucleic acids, proteins and antibodies of the invention are labeled. By "labeled" herein is meant that a compound has at least one element, isotope or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies or antigens; and c) colored or fluorescent dyes. The labels may be incorporated into the breast cancer nucleic acids, proteins and antibodies at any position. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^{3}H, ^{14}C, ^{32}P, ^{35}S, or ^{125}I, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-

galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Accordingly, the present invention also provides breast cancer protein sequences. A breast cancer protein of the present invention may be identified in several ways. "Protein" in this sense includes proteins, polypeptides, and peptides. As will be appreciated by those in the art, the nucleic acid sequences of the invention can be used to generate protein sequences. There are a variety of ways to do this, including cloning the entire gene and verifying its frame and amino acid sequence, or by comparing it to known sequences to search for homology to provide a frame, assuming the breast cancer protein has homology to some protein in the database being used. Generally, the nucleic acid sequences are input into a program that will search all three frames for homology. This is done in a preferred embodiment using the following NCBI Advanced BLAST parameters. The program is blastx or blastn. The database is nr. The input data is as "Sequence in FASTA format". The organism list is "none". The "expect" is 10; the filter is default. The "descriptions" is 500, the "alignments" is 500, and the "alignment view" is pairwise. The "Query Genetic Codes" is standard (1). The matrix is BLOSUM62; gap existence cost is 11, per residue gap cost is 1; and the lambda ratio is .85 default. This results in the generation of a putative protein sequence.

Also included within one embodiment of breast cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques known in the art as are outlined above for the nucleic acid homologies.

Breast cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of breast cancer proteins are portions or fragments of the wild type sequences. herein. In addition, as outlined above, the breast cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence, using techniques known in the art.

In a preferred embodiment, the breast cancer proteins are derivative or variant breast cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative breast cancer peptide will contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the breast cancer peptide.

Also included in an embodiment of breast cancer proteins of the present invention are amino acid sequence variants. These variants fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the breast cancer protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant breast cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the breast cancer protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed breast cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of breast cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small

alterations in the characteristics of the breast cancer protein are desired, substitutions are generally made in accordance with the following chart:

Chart I

Original Residue	Exemplary Substitutions
Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Asn, Gln
Ile	Leu, Val
Leu	Ile, Val
Lys	Arg, Gln, Glu
Met	Leu, Ile
Phe	Met, Leu, Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp, Phe
Val	Ile, Leu

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those shown in Chart I. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analogue, although variants also are selected to modify the characteristics of the breast cancer proteins as needed. Alternatively, the variant may be designed

such that the biological activity of the breast cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of breast cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a breast cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a breast cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking breast cancer to a water-insoluble support matrix or surface for use in the method for purifying anti-breast cancer antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidyl-propionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the breast cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence breast cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence breast cancer polypeptide.

Addition of glycosylation sites to breast cancer polypeptides may be accomplished by altering the amino acid sequence thereof. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence breast cancer polypeptide (for O-linked glycosylation sites). The breast cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the breast

cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the breast cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, breast cancer Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the breast cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of breast cancer comprises linking the breast cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

Breast cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a breast cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a breast cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the breast cancer polypeptide. The presence of such epitope-tagged forms of a breast cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the breast cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a breast cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

Also included with the definition of breast cancer protein in one embodiment are other breast cancer proteins of the breast cancer family, and breast cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related breast cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the breast cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art.

In addition, as is outlined herein, breast cancer proteins can be made that are longer than those depicted in the figures, for example, by the elucidation of additional sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Breast cancer proteins may also be identified as being encoded by breast cancer nucleic acids. Thus, breast cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

In a preferred embodiment, when the breast cancer protein is to be used to generate antibodies, for example for immunotherapy, the breast cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller breast cancer protein will be able to bind to the full length protein. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a

unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from BCH1p1, BCH1p2, BCR3p1, BCR3p2, BCQ8p1, BCQ8p2, BCQ5p1, BCQ5p2, BCN1p1, BCN1p2, wherein BCH1p1 and BCH1p2 are preferred. In one embodiment the epitope or fragment of BCH1p1 is conjugated to KLH or BSA.

In one embodiment, the term "antibody" includes antibody fragments, as are known in the art, including Fab, Fab_2, single chain antibodies (Fv for example), chimeric antibodies, etc., either produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA technologies.

Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the BCH1 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include the BCH1 polypeptide or fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or

mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the breast cancer protein or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific.

In a preferred embodiment, the antibodies to breast cancer are capable of reducing or eliminating the biological function of breast cancer, as is described below. That is, the addition of anti-breast cancer antibodies (either polyclonal or preferably monoclonal) to breast cancer (or cells containing breast cancer) may reduce or eliminate the breast cancer activity. Generally, at least a 25% decrease in activity is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the breast cancer proteins are humanized antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will

comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., Bio/Technology 10, 779-783 (1992); Lonberg et al., Nature 368 856-859 (1994); Morrison, Nature 368, 812-13 (1994); Fishwild et al., Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995).

By immunotherapy is meant treatment of breast cancer with an antibody raised against breast cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as

defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen.

In a preferred embodiment the breast cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted breast cancer protein.

In another preferred embodiment, the breast cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the breast cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane breast cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the breast cancer protein. The antibody is also an antagonist of the breast cancer protein. Further, the antibody prevents activation of the transmembrane breast cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the breast cancer protein, the antibody prevents growth of the cell. The antibody also sensitizes the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity. Thus, breast cancer is treated by administering to a patient antibodies directed against the transmembrane breast cancer protein.

In another preferred embodiment, the antibody is conjugated to a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the breast cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the breast cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or protein kinase activity associated with breast cancer.

In a preferred embodiment, the therapeutic moiety may also be a cytotoxic agent. In this method, targeting the cytotoxic agent to tumor tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with breast cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diptheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against breast cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane breast cancer proteins not only serves to increase the local concentration of therapeutic moiety in the breast cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

The breast cancer antibodies of the invention specifically bind to breast cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a binding constant in the range of at least 10^{-4}- 10^{-6} M^{-1}, with a preferred range being 10^{-7} - 10^{-9} M^{-1}.

In a preferred embodiment, the breast cancer protein is purified or isolated after expression. Breast cancer proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the breast cancer protein may be purified using a standard anti-breast cancer antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, R., Protein Purification, Springer-Verlag, NY (1982). The degree of purification necessary will vary depending on the use of the breast cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the breast cancer proteins and nucleic acids are useful in a number of applications.

In one aspect, the expression levels of genes are determined for different cellular states in the breast cancer phenotype; that is, the expression levels of genes in normal breast tissue and in breast cancer tissue (and in some cases, for varying severities of breast cancer that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or

point of development is essentially a "fingerprint" of the state; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be done or confirmed: does tissue from a particular patient have the gene expression profile of normal or breast cancer tissue.

"Differential expression," or grammatical equivalents as used herein, refers to both qualitative as well as quantitative differences in the genes' temporal and/or cellular expression patterns within and among the cells. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, for example, normal versus breast cancer tissue. That is, genes may be turned on or turned off in a particular state, relative to another state. As is apparent to the skilled artisan, any comparison of two or more states can be made. Such a qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques in one such state or cell type, but is not detectable in both. Alternatively, the determination is quantitative in that expression is increased or decreased; that is, the expression of the gene is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, Nature Biotechnology, 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e. upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably, at least about 200%, with from 300 to at least 1000% being especially preferred.

As will be appreciated by those in the art, this may be done by evaluation at either the gene transcript, or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, for example through the use of antibodies to the breast cancer protein and standard immunoassays (ELISAs,e tc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Thus, the

proteins corresponding to breast cancer genes, i.e. those identified as being important in a breast cancer phenotype, can be evaluated in a breast cancer diagnostic test.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well. Similarly, these assays may be done on an individual basis as well.

In this embodiment, the breast cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of breast cancer sequences in a particular cell. The assays are further described below in the example.

In a preferred embodiment nucleic acids encoding the breast cancer protein are detected. Although DNA or RNA encoding the breast cancer protein may be detected, of particular interest are methods wherein the mRNA encoding a breast cancer protein is detected. The presence of mRNA in a sample is an indication that the breast cancer gene has been transcribed to form the mRNA, and suggests that the protein is expressed. Probes to detect the mRNA can be any nucleotide/deoxynucleotide probe that is complementary to and base pairs with the mRNA and includes but is not limited to oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a breast cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, any of the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing breast cancer sequences are used in diagnostic assays. This can be done on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput

screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, breast cancer proteins, including intracellular, transmembrane or secreted proteins, find use as markers of breast cancer. Detection of these proteins in putative breast cancer tissue or patients allows for a determination or diagnosis of breast cancer. Numerous methods known to those of ordinary skill in the art find use in detecting breast cancer. In one embodiment, antibodies are used to detect breast cancer proteins. A preferred method separates proteins from a sample or patient by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be any other type of gel including isoelectric focusing gels and the like). Following separation of proteins, the breast cancer protein is detected by immunoblotting with antibodies raised against the breast cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the breast cancer protein find use in in situ imaging techniques. In this method cells are contacted with from one to many antibodies to the breast cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the breast cancer protein(s) contains a detectable label. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a pluralilty of breast cancer proteins. As will be appreciated by one of ordinary skill in the art, numerous other histological imaging techniques are useful in the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing breast cancer from blood samples. As previously described, certain breast cancer proteins are secreted/circulating molecules. Blood samples, therefore, are useful as samples to be probed or tested for the presence of secreted breast cancer proteins. Antibodies can be used to detect the breast cancer by any of the previously described immunoassay techniques including ELISA, immunoblotting (Western blotting), immunoprecipitation, BIACORE technology and the like, as will be appreciated by one of ordinary skill in the art.

In a preferred embodiment, in situ hybridization of labeled breast cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including breast cancer tissue and/or normal tissue, are made. In situ hybridization as is known in the art can then be done.

It is understood that when comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis as well as a prognosis. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis.

In a preferred embodiment, the breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing breast cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to breast cancer severity, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, the breast cancer probes are attached to biochips for the detection and quantification of breast cancer sequences in a tissue or patient. The assays proceed as outlined for diagnosis.

In a preferred embodiment, any of the three classes of proteins as described herein are used in drug screening assays. The breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing breast cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, Zlokarnik, et al., Science 279, 84-8 (1998), Heid, 1996 #69.

In a preferred embodiment, the breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified breast cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the breast cancer phenotype. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in breast cancer, candidate bioactive agents may be screened to modulate this gene's response; preferably to down regulate the gene, although in some circumstances to up regulate the gene. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tumor tissue, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4 fold increase in tumor compared to normal tissue, a decrease of about four fold is desired; a 10 fold decrease in tumor compared to normal tissue gives a 10 fold increase in expression for a candidate agent is desired.

As will be appreciated by those in the art, this may be done by evaluation at either the gene or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, for example through the use of antibodies to the breast cancer protein and standard immunoassays.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well.

In this embodiment, the breast cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of breast cancer sequences in a particular cell. The assays are further described below.

Generally, in a preferred embodiment, a candidate bioactive agent is added to the cells prior to analysis. Moreover, screens are provided to identify a candidate bioactive agent which modulates breast cancer, modulates breast cancer proteins, binds to a breast cancer protein, or interferes between the binding of a breast cancer protein and an antibody.

The term "candidate bioactive agent" or "drug candidate" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for bioactive agents that are capable of directly or indirectly altering either the breast cancer phenotype or the expression of a breast cancer sequence, including both

nucleic acid sequences and protein sequences. In preferred embodiments, the bioactive agents modulate the expression profiles, or expression profile nucleic acids or proteins provided herein. In a particularly preferred embodiment, the candidate agent suppresses a breast cancer phenotype, for example to a normal breast tissue fingerprint. Similarly, the candidate agent preferably suppresses a severe breast cancer phenotype. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification to produce structural analogs.

In a preferred embodiment, the candidate bioactive agents are proteins. By "protein" herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. The protein may be made up of naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures. Thus "amino acid", or "peptide residue", as used herein means

both naturally occurring and synthetic amino acids. For example, homo-phenylalanine, citrulline and noreleucine are considered amino acids for the purposes of the invention. "Amino acid" also includes imino acid residues such as proline and hydroxyproline. The side chains may be in either the (R) or the (S) configuration. In the preferred embodiment, the amino acids are in the (S) or L-configuration. If non-naturally occurring side chains are used, non-amino acid substituents may be used, for example to prevent or retard in vivo degradations.

In a preferred embodiment, the candidate bioactive agents are naturally occurring proteins or fragments of naturally occurring proteins. Thus, for example, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of procaryotic and eucaryotic proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred.

In a preferred embodiment, the candidate bioactive agents are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, for example, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

In a preferred embodiment, the candidate bioactive agents are nucleic acids, as defined above.

As described above generally for proteins, nucleic acid candidate bioactive agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate bioactive agents are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing the target sequences to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR occurring as needed, as will be appreciated by those in the art. For example, an in vitro transcription with labels covalently attached to the nucleosides is done. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, for example, a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. As known in the art, unbound labeled streptavidin is removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared

as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways, as will be appreciated by those in the art. Components of the reaction may be added simultaneously, or sequentially, in any order, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents may be included in the assays. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used, depending on the sample preparation methods and purity of the target.

Once the assay is run, the data is analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

The screens are done to identify drugs or bioactive agents that modulate the breast cancer phenotype. Specifically, there are several types of screens that can be run. A preferred embodiment is in the screening of candidate agents that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. That is, candidate agents that can mimic or produce an expression profile in breast cancer similar to the expression profile of normal breast tissue is expected to result in a suppression of the breast cancer phenotype. Thus, in this embodiment, mimicking an expression profile, or changing one profile to another, is the goal.

In a preferred embodiment, as for the diagnosis and prognosis applications, having identified the differentially expressed genes important in any one state, screens can be run to alter the expression of the genes individually. That is, screening for modulation of regulation of expression of a single gene can be done; that is, rather than try to mimic all or part of an expression profile, screening for regulation of individual genes can be done. Thus, for example, particularly in the case of target genes whose presence or absence is unique between two states, screening is done for modulators of the target gene expression.

In a preferred embodiment, screening is done to alter the biological function of the expression product of the differentially expressed gene. Again, having identified the importance of a gene in a particular state, screening for agents that bind and/or modulate the biological activity of the gene product can be run as is more fully outlined below.

Thus, screening of candidate agents that modulate the breast cancer phenotype either at the gene expression level or the protein level can be done.

In addition screens can be done for novel genes that are induced in response to a candidate agent. After identifying a candidate agent based upon its ability to suppress a breast cancer expression pattern leading to a normal expression pattern, or modulate a single breast cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated breast cancer tissue reveals genes that are not expressed in normal tissue or breast cancer tissue, but are expressed in agent treated tissue. These agent specific sequences can be identified and used by any of the methods described herein for breast cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated breast cancer tissue sample.

Thus, in one embodiment, a candidate agent is administered to a population of breast cancer cells, that thus has an associated breast cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e. a peptide) may be

put into a viral construct such as a retroviral construct and added to the cell, such that expression of the peptide agent is accomplished; see PCT US97/01019, hereby expressly incorporated by reference.

Once the candidate agent has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, for example, breast cancer tissue may be screened for agents that reduce or suppress the breast cancer phenotype. A change in at least one gene of the expression profile indicates that the agent has an effect on breast cancer activity. By defining such a signature for the breast cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "breast cancer proteins", "breast cancer modulating proteins" "BCP" or a "BCMP". In one embodiment, BCMP is termed BCH1. In one embodiment, BCH1 can be identified as described for identifying breast cancer proteins herein. In a preferred embodiment, BCH1 is depicted in Figure 34. The BCMP may be a fragment, or alternatively, be the full length protein to the fragment shown herein. Preferably, the BCMP is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment.

In other preferred embodiments herein, the breast cancer protein or nucleic acid encoding a breast cancer protein may be selected from any sequence provided in the figures including those wherein the accession numbers are provided. Preferred sequences are in Figure 10, more preferably Figure 11 and most preferably Figure 12. Preferred sequences are also selected from the group consisting of BCH1, BCA2, BCJ7, BCN1, BCN5, BCO2, BCQ5, BCR2, BCR3, BCQ8, BCN2, BCX3, BCX2 and BCY3. Most preferably, the sequence is selected from the group consisting of BCH1, BCA2, BCJ7, BCN1, BCN5, BCO2, BCQ5, BCR2, BCX2 and BCY3. It is understood that any protein can also be

selected from any subset of this group of proteins, for example, BCH1 can be selected from the whole group, or from the subset of BCH1 and BCN1.

In one embodiment the breast cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the breast cancer protein is conjugated to BSA.

Thus, in a preferred embodiment, screening for modulators of expression of specific genes can be done. This will be done as outlined above, but in general the expression of only one or a few genes are evaluated.

In a preferred embodiment, screens are designed to first find candidate agents that can bind to differentially expressed proteins, and then these agents may be used in assays that evaluate the ability of the candidate agent to modulate differentially expressed activity. Thus, as will be appreciated by those in the art, there are a number of different assays which may be run; binding assays and activity assays.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. In general, this is done as is known in the art. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the breast cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a breast cancer protein and a candidate bioactive agent, and determining the binding of the candidate agent to the breast cancer protein. Preferred embodiments utilize the human breast cancer protein, although other mammalian proteins may also be used, for example for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative breast cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the breast cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates,

arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the breast cancer protein is bound to the support, and a candidate bioactive agent is added to the assay. Alternatively, the candidate agent is bound to the support and the breast cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the candidate bioactive agent to the breast cancer protein may be done in a number of ways. In a preferred embodiment, the candidate bioactive agent is labelled, and binding determined directly. For example, this may be done by attaching all or a portion of the breast cancer protein to a solid support, adding a labelled candidate agent (for example a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as is known in the art.

By "labeled" herein is meant that the compound is either directly or indirectly labeled with a label which provides a detectable signal, e.g. radioisotope, fluorescers, enzyme, antibodies, particles such as magnetic particles, chemiluminescers, or specific binding molecules, etc. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin etc. For the specific binding members, the complementary member would normally be labeled with a molecule which provides for

detection, in accordance with known procedures, as outlined above. The label can directly or indirectly provide a detectable signal.

In some embodiments, only one of the components is labeled. For example, the proteins (or proteinaceous candidate agents) may be labeled at tyrosine positions using ^{125}I, or with fluorophores. Alternatively, more than one component may be labeled with different labels; using ^{125}I for the proteins, for example, and a fluorophor for the candidate agents.

In a preferred embodiment, the binding of the candidate bioactive agent is determined through the use of competitive binding assays. In this embodiment, the competitor is a binding moiety known to bind to the target molecule (i.e. breast cancer), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding as between the bioactive agent and the binding moiety, with the binding moiety displacing the bioactive agent.

In one embodiment, the candidate bioactive agent is labeled. Either the candidate bioactive agent, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at any temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are selected for optimum activity, but may also be optimized to facilitate rapid high through put screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the candidate bioactive agent. Displacement of the competitor is an indication that the candidate bioactive agent is binding to the breast cancer protein and thus is capable of binding to, and potentially modulating, the activity of the breast cancer protein. In this embodiment, either component can be labeled. Thus, for example, if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the candidate bioactive agent is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the candidate bioactive agent is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the bioactive agent is bound to the breast cancer protein with a higher affinity. Thus, if the candidate

bioactive agent is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the candidate agent is capable of binding to the breast cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity bioactive agents that are capable of modulating the activity of the breast cancer proteins. In this embodiment, the methods comprise combining a breast cancer protein and a competitor in a first sample. A second sample comprises a candidate bioactive agent, a breast cancer protein and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the breast cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the breast cancer protein.

Alternatively, a preferred embodiment utilizes differential screening to identify drug candidates that bind to the native breast cancer protein, but cannot bind to modified breast cancer proteins. The structure of the breast cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect breast cancer bioactivity are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably all control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, all samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding.

Screening for agents that modulate the activity of breast cancer proteins may also be done. In a preferred embodiment, methods for screening for a bioactive agent capable of modulating the activity

of breast cancer proteins comprise the steps of adding a candidate bioactive agent to a sample of breast cancer proteins, as above, and determining an alteration in the biological activity of breast cancer proteins. "Modulating the activity of breast cancer" includes an increase in activity, a decrease in activity, or a change in the type or kind of activity present. Thus, in this embodiment, the candidate agent should both bind to breast cancer proteins (although this may not be necessary), and alter its biological or biochemical activity as defined herein. The methods include both in vitro screening methods, as are generally outlined above, and in vivo screening of cells for alterations in the presence, distribution, activity or amount of breast cancer proteins.

Thus, in this embodiment, the methods comprise combining a breast cancer sample and a candidate bioactive agent, and evaluating the effect on breast cancer activity. By "breast cancer activity" or grammatical equivalents herein is meant one of the breast cancer's biological activities, including, but not limited to, cell division, preferably in breast tissue, cell proliferation, tumor growth, transformation of cells. In one embodiment, breast cancer activity include activation of breast cancer protein, BCH1, for example, or a substrate thereof by the breast cancer protein. An inhibitor of breast cancer activity is the inhibition of any one or more breast cancer activities.

In a preferred embodiment, the activity of the breast cancer protein is increased; in another preferred embodiment, the activity of the breast cancer protein is decreased. Thus, bioactive agents that are antagonists are preferred in some embodiments, and bioactive agents that are agonists may be preferred in other embodiments.

In a preferred embodiment, the invention provides methods for screening for bioactive agents capable of modulating the activity of a breast cancer protein. The methods comprise adding a candidate bioactive agent, as defined above, to a cell comprising breast cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a breast cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, for example hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, bioactive agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the breast cancer protein. In one embodiment, "breast cancer protein activity" as used herein includes at least one of the following: breast cancer activity, binding to a breast cancer protein, activation of a breast cancer protein or activation of substrates of a breast cancer protein by a breast cancer protein.

In one embodiment, a method of inhibiting breast cancer cell division is provided. The method comprises administration of a breast cancer inhibitor.

Neutralizing means that activity of a protein is either inhibited or counter acted against so as to have substantially no effect on the cell.

In another embodiment, a method of inhibiting tumor growth is provided. The method comprises administration of a breast cancer inhibitor.

In a further embodiment, methods of treating cells or individuals with cancer are provided. The method comprises administration of a breast cancer inhibitor.

In one embodiment, a breast cancer inhibitor is an antibody as discussed above. In another embodiment, the breast cancer inhibitor is an antisense molecule. Antisense molecules as used herein include antisense or sense oligonucleotides comprising a singe-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for breast cancer molecules. A preferred antisense molecule is for BCH1 or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Antisense molecules may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind

to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

The compounds having the desired pharmacological activity may be administered in a physiologically acceptable carrier to a host, as previously described. The agents may be administered in a variety of ways, orally, parenterally e.g., subcutaneously, intraperitoneally, intravascularly, etc. Depending upon the manner of introduction, the compounds may be formulated in a variety of ways. The concentration of therapeutically active compound in the formulation may vary from about 0.1-100 wt.%. The agents may be administered alone or in combination with other treatments, i.e., radiation.

The pharmaceutical compositions can be prepared in various forms, such as granules, tablets, pills, suppositories, capsules, suspensions, salves, lotions and the like. Pharmaceutical grade organic or inorganic carriers and/or diluents suitable for oral and topical use can be used to make up compositions containing the therapeutically-active compounds. Diluents known to the art include aqueous media, vegetable and animal oils and fats. Stabilizing agents, wetting and emulsifying agents, salts for varying the osmotic pressure or buffers for securing an adequate pH value, and skin penetration enhancers can be used as auxiliary agents.

Without being bound by theory, it appears that the various breast cancer sequences are important in breast cancer. Accordingly, disorders based on mutant or variant breast cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant breast cancer genes comprising determining all or part of the sequence of at least one endogeneous breast cancer genes in a cell. As will be appreciated by those in the art, this may be done using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the breast cancer genotype of an individual comprising determining all or part of the sequence of at least one breast cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced breast cancer gene to a known breast cancer gene, i.e. a wild-type gene.

The sequence of all or part of the breast cancer gene can then be compared to the sequence of a known breast cancer gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a a difference in the sequence between the breast cancer gene of the patient and the known breast cancer gene is indicative of a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the breast cancer genes are used as probes to determine the number of copies of the breast cancer gene in the genome.

In another preferred embodiment breast cancer genes are used as probed to determine the chromosomal localization of the breast cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in breast cancer gene loci.

Thus, in one embodiment, methods of modulating breast cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-breast cancer antibody that reduces or eliminates the biological activity of an endogenous breast cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a breast cancer protein. As will be appreciated by those in the art, this may be accomplished in any number of ways. In a preferred embodiment, for example when the breast cancer sequence is down-regulated in breast cancer, the activity of the breast cancer gene is increased by increasing the amount of breast cancer in the cell, for example by overexpressing the endogenous breast cancer or by administering a gene encoding the breast cancer sequence, using known gene-therapy techniques, for example. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), for example as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, for example when the breast cancer sequence is up-regulated in breast cancer, the activity of the endogeneous breast cancer gene is decreased, for example by the administration of a breast cancer antisense nucleic acid.

In one embodiment, the breast cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to breast cancer proteins, which are useful as described herein. Similarly, the breast cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify breast cancer antibodies. In a preferred embodiment, the antibodies are generated to epitopes unique to a breast cancer protein;

that is, the antibodies show little or no cross-reactivity to other proteins. These antibodies find use in a number of applications. For example, the breast cancer antibodies may be coupled to standard affinity chromatography columns and used to purify breast cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the breast cancer protein.

In one embodiment, a therapeutically effective dose of a breast cancer or modulator thereof is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. As is known in the art, adjustments for protein degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals, and organisms. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, and in the most preferred embodiment the patient is human.

The administration of the breast cancer proteins and modulators of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the breast cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a breast cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as

acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol. Additives are well known in the art, and are used in a variety of formulations.

In a preferred embodiment, breast cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, breast cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the breast cancer coding regions) can be administered in gene therapy applications, as is known in the art. These breast cancer genes can include antisense applications, either as gene therapy (i.e. for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

In a preferred embodiment, breast cancer genes are administered as DNA vaccines, either single genes or combinations of breast cancer genes. Naked DNA vaccines are generally known in the art. Brower, Nature Biotechnology, 16:1304-1305 (1998).

In one embodiment, breast cancer genes of the present invention are used as DNA vaccines. Methods for the use of genes as DNA vaccines are well known to one of ordinary skill in the art, and include placing a breast cancer gene or portion of a breast cancer gene under the control of a promoter for expression in a breast cancer patient. The breast cancer gene used for DNA vaccines can encode full-length breast cancer proteins, but more preferably encodes portions of the breast cancer proteins including peptides derived from the breast cancer protein. In a preferred embodiment a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived

from a breast cancer gene. Similarly, it is possible to immunize a patient with a plurality of breast cancer genes or portions thereof as defined herein. Without being bound by theory, expression of the polypeptide encoded by the DNA vaccine, cytotoxic T-cells, helper T-cells and antibodies are induced which recognize and destroy or eliminate cells expressing breast cancer proteins.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the breast cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are known to those of ordinary skill in the art and find use in the invention.

In another preferred embodiment breast cancer genes find use in generating animal models of breast cancer. As is appreciated by one of ordinary skill in the art, when the breast cancer gene identified is repressed or diminished in breast cancer tissue, gene therapy technology wherein antisense RNA directed to the breast cancer gene will also diminish or repress expression of the gene. An animal generated as such serves as an animal model of breast cancer that finds use in screening bioactive drug candidates. Similarly, gene knockout technology, for example as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence of the breast cancer protein. When desired, tissue-specific expression or knockout of the breast cancer protein may be necessary.

It is also possible that the breast cancer protein is overexpressed in breast cancer. As such, transgenic animals can be generated that overexpress the breast cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of breast cancer and are additionally useful in screening for bioactive molecules to treat breast cancer.

It is understood that the examples described herein in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references and sequences of accession numbers cited herein are incorporated by reference in their entirety.

EXAMPLE

Expression studies were performed herein on both the protein and nucleic acid level. Results are provided in the figures.

An experiment was performed to examine the correlation (if any) between BCH1 protein and estrogen receptor (ER) expression and localization. Antibodies against BCH1 protein were obtained by immunization in rabbits with 15-mer synthetic peptides corresponding to regions of BCH1. Anti-ER antibodies were purchased commercially. Approximately 50 breast carcinoma tissue specimens (5 micron serial sections; paraffin-embedded, formalin-fixed) were analyzed by immunohistochemistry. Of these, ~40% were positive for BCH1 expression; ~35% were positive for ER. Protein levels were scored from 1 to 5 by immunohistochemistry, with 5 representing the highest expression. Co-expression of BCH1 and ER is shown in Figure 37.

Of the ER+ tumors (n=108), about one-half have predominantly nuclear localizations of ER, one-half predominantly cytoplasmic. Interestingly, while the BCH1+/ER+ tumors were no more prevalent than by chance, without exception tumors with high levels of BCH1 (IHC score = 4 or 5) showed exclusively localization of ER to the cytoplasm, with exclusion from the nucleus (see Figures 38 and 39) (n=16, $p<5 \times 10^{-7}$), whereas low expression of BCH1 had no correlation with ER localization and was often associated with nuclear ER (see Figures 40 and 41).

Currently, ER expression is an important clinical prognostic marker for breast cancer. Because signaling through ER to activate most estrogen-responsive genes is believed to require translocation of activated ER to the nucleus, high expression of BCH1 is predicted to correlate with functionally-negative ER in ER+ tumors. Since ER- correlates with poor prognosis, BCH1 may also be a valuable prognostic marker, as it may also correlate with poor prognosis, or to no-responsiveness to anti-estrogen therapies (e.g., tamoxifen), since approximately 50% of the ER+ patients do not respond to tamoxifen. Tamoxifen works against the effects of estrogen on these cells. It is often called an "anti-estrogen." As a treatment for breast cancer, the drug slows or stops the growth of cancer cells that are already present in the body. As adjuvant therapy, tamoxifen has been shown to help prevent the original breast cancer from returning and also prevent the development of new cancers in the opposite breast.

Recent publications report that ER can signal through the Ras/Raf/MAP kinase. Since many of the proteins in this signaling cascade reside in the cytoplasm, increased BCH1 expression may correlate with, or even cause, ER to remain in the cytoplasm, thereby altering the signaling of ER through the

MAP kinase pathway. This may be an explanation for the subset of ER+ patients who do not respond to tamoxifen.

Furthermore, BCH1 may have a casual role in ER translocation to the nucleus, by either directly or indirectly preventing nuclear translocation, thereby eliminating or altering responsiveness of the cell to estrogens or their analogs.

CLAIMS

We claim:

1. A method of screening drug candidates comprising:
a) providing a cell that expresses an expression profile gene which encodes a protein selected from the group consisting of BCH1, BCA2, BCJ7, BCN1, BCN5, BCO2, BCQ5, BCR2, BCX2 and BCY3 or a fragment thereof;
b) adding a drug candidate to said cell; and
c) determining the effect of said drug candidate on the expression of said expression profile gene.

2. A method according to claim 1 wherein said determining comprises comparing the level of expression in the absence of said drug candidate to the level of expression in the presence of said drug candidate, wherein the concentration of said drug candidate can vary when present, and wherein said comparison can occur after addition or removal of the drug candidate.

3. A method according to claim 1 wherein the expression of said profile gene is decreased as a result of the introduction of the drug candidate.

4. A method of screening for a bioactive agent capable of binding to a breast cancer modulator protein (BCMP), wherein said BCMP is BCH1 or a fragment thereof, said method comprising combining said BCMP and a candidate bioactive agent, and determining the binding of said candidate agent to said BCMP.

5. A method for screening for a bioactive agent capable of modulating the activity of a breast cancer modulator protein (BCMP), wherein said BCMP is BCH1 or a fragment thereof, said method comprising combining said BCMP and a candidate bioactive agent, and determining the effect of said candidate agent on the bioactivity of said BCMP.

6. A method of evaluating the effect of a candidate breast cancer drug comprising:
a) administering said drug to a patient;
b) removing a cell sample from said patient; and
c) determining the expression profile of said cell.

7. A method according to claim 6 further comprising comparing said expression profile to an expression profile of a healthy individual.

8. A biochip comprising a nucleic acid segment encoding BCH1 or a fragment thereof, wherein said biochip comprises fewer than 1000 nucleic acid probes.

9. A method of diagnosing breast cancer comprising:

a) determining the expression of a gene encoding BCH1 or a fragment thereof in a first tissue type of a first individual; and

b) comparing said expression of said gene from a second normal tissue type from said first individual or a second unaffected individual;

wherein a difference in said expression indicates that the first individual has breast cancer.

10. An antibody which specifically binds to BCH1, or a fragment thereof.

11. The antibody of Claim 10 wherein said fragment is BCH1p1 or BCH1p2.

12. The antibody of Claim 10, wherein said antibody is a monoclonal antibody.

13. The antibody of Claim 10, wherein said antibody is a humanized antibody.

14. The antibody of Claim 10, wherein said antibody is an antibody fragment.

15. A method for screening for a bioactive agent capable of interfering with the binding of a breast cancer modulator protein (BCMP) or a fragment thereof and an antibody which binds to said BCMP or fragment thereof, said method comprising:

a) combining a BCMP or fragment thereof, a candidate bioactive agent and and an antibody which binds to said BCMP or fragment thereof; and

b) determining the binding of said BCMP or fragment thereof and said antibody.

16. A method for inhibiting breast cancer, said method comprising administering to a cell a composition comprising an antibody to BCH1 or a fragment thereof.

17. The method of Claim 16 wherein said cell is a cell of an individual.

18. The method of Claim 17 wherein said individual has cancer.

19. The method of Claim 16 wherein said fragment is selected from the group consisting of BCH1p1 and BCH1p2.

20. The method of Claim 16 wherein said antibody is a humanized antibody.

21. The method of Claim 16 wherein said antibody is an antibody fragment.

22. A method for inhibiting breast cancer in a cell, wherein said method comprises administering to a cell a composition comprising antisense molecules to BCH1.

23. A peptide consisting essentially of BCH1p1.

24. A composition comprising the peptide of Claim 23.

25. A peptide consisting essentially of BCH1p2.

26. A composition comprising the peptide of Claim 25.

27. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising BCH1 or a fragment thereof.

28. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising a nucleic acid comprising a sequence encoding BCH1 or a fragment thereof.

29. A composition capable of eliciting an immune response in an individual, said composition comprising BCH1 or a fragment thereof and a pharmaceutically acceptable carrier.

30. A composition capable of eliciting an immune response in an individual, said composition comprising a nucleic acid comprising a sequence encoding BCH1 or a fragment thereof and a pharmaceutically acceptable carrier.

31. A method of treating an individual for breast cancer comprising administering to said individual an inhibitor of BCH1.

32. The method of Claim 31 wherein said inhibitor is an antibody.

33. The method of Claim 31 wherein said individual is non-responsive to an anti-estrogen and is positive for estrogen receptor.

34. The method of Claim 33 wherein said method further comprises administering an anti-estrogen.

35. A method for determining the prognosis of an individual with breast cancer comprising determining the level of BCH1 in a sample, wherein a high level of BCH1 indicates a poor prognosis.

36. A method for determining whether an individual with breast cancer will be non-responsive to anti-estrogen therapies comprising determining the level of BCH1 wherein a high level of BCH1 indicates that an individual will be non-responsive.

37. A method of neutralizing the effect of a BCH1, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization.

FIGURE 1

Affymetrix ID	Accession	Gene Name	Ratio breast v. tumor
RC_AA025277	AA025277	ESTs	10.0
RC_H49425	H49425	ESTs	10.0
RC_N51657	N51657	EST	10.0
RC_R16733	R16733	ESTs	10.0
RC_AA079072_	AA079072	Insulin-like growth factor binding protein 6	10.0
HG1428-HT1428	TIGR - HG1428-HT1428	EST - HG1428-HT1428	10.0
HG2157-HT2227	TIGR - HG2157-HT2227	EST - HG2157-HT2227	10.0
HG2841-HT2969	TIGR - HG2841-HT2969	EST - HG2841-HT2969	10.0
J02874	J02874	Fatty acid binding protein 4 adipocyte	10.0
J03474	J03474	SERUM AMYLOID A PROTEIN PRECURSOR	10.0
L19871	L19871	Activating transcription factor 3	10.0
L49169	L49169	Human G0S3 mRNA complete cds	10.0
M12963	M12963	Alcohol dehydrogenase 1 (class I) alpha polypeptide	10.0
M21305	M21305	EST - M21305	10.0
M22430	M22430	Phospholipase A2 group IIA (platelets synovial	10.0
M25079	M25079	Hemoglobin beta	10.0
M27826	M27826	Human endogenous retroviral protease mRNA	10.0
M30185	M30185	Cholesteryl ester transfer protein plasma	10.0
U22961	U22961	EST - U22961	10.0
U48251	U48251	Homo sapiens protein kinase C-binding protein	10.0
U88902_cds1_f	U88902	EST - U88902_cds1_f	10.0
X00129	X00129	PLASMA RETINOL-BINDING PROTEIN	10.0
X04602	X04602	Interleukin 6 (B cell stimulatory factor 2)	10.0
X51441	X51441	SERUM AMYLOID A PROTEIN PRECURSOR	10.0
X64559	X64559	Tetranectin (plasminogen-binding protein)	10.0
X75958	X75958	TrkB (alternatively spliced) [human brain mRNA	10.0
X87344_cds10_r	X87344	H.sapiens DMA DMB HLA-Z1 IPP2 LMP2 TAP1	10.0
X99142	X99142	H.sapiens mRNA for hHKb1 protein	10.0
Z49269	Z49269	Homo sapiens MIP-1 delta mRNA complete cds	10.0
AA081995	AA081995	EST - AA081995	10.0
AA090439	AA090439	ESTs	10.0
AA137107	AA137107	ESTs	10.0
AA203296	AA203296	ESTs	10.0
AA285284	AA285284	ESTs Highly similar to ISOCITRATE	10.0
AA310850	AA310850	ESTs	10.0

FIGURE 1 (CONT.)

AA418143	AA418143	ESTs	10.0
AA425719	AA425719	ESTs	10.0
AA427379	AA427379	ESTs	10.0
AA452705	AA452705	ESTs Weakly similar to D2045.9 [C.elegans]	10.0
AB002328	AB002328	Human mRNA for KIAA0330 gene partial cds	10.0
AF000575_s	AF000575	Homo sapiens clone 17.11 immunoglobulin-like	10.0
M12272_s	M12272	Alcohol dehydrogenase 3 (class I) gamma	10.0
M26315_cds2_s	M26315	CD8 antigen alpha polypeptide (p32)	10.0
M64936_i	M64936	Homo sapiens retinoic acid-inducible endogenous	10.0
M81349	M81349	SERUM AMYLOID A-4 PROTEIN PRECURSOR	10.0
M84526	M84526	D component of complement (adipsin)	10.0
N73185	N73185	EST	10.0
N79674_s	N79674	ESTs	10.0
N88827	N88827	ESTs	10.0
N91071_s	N91071	ESTs	10.0
R21149	R21149	ESTs Highly similar to RAB GDP	10.0
R69417	R69417	ESTs	10.0
RC_AA009764	AA009764	ESTs	10.0
RC_AA017254	AA017254	ESTs	10.0
RC_AA019300	AA019300	ESTs	10.0
RC_AA026280	AA026280	ESTs	10.0
RC_AA115253	AA115253	ESTs	10.0
RC_AA128617	AA128617	ESTs	10.0
RC_AA179338	AA179338	ESTs Moderately similar to retrovirus-related pol	10.0
RC_AA223237	AA223237	ESTs	10.0
RC_AA234308	AA234308	H.sapiens mRNA for HES1 protein	10.0
RC_AA251772	AA251772	Homo sapiens mRNA for HsGAK complete cds	10.0
RC_AA279673	AA279673	ESTs	10.0
RC_AA411443	AA411443	ESTs	10.0
RC_AA416947	AA416947	ESTs	10.0
RC_AA426584	AA426584	ESTs	10.0
RC_AA434113	AA434113	ESTs	10.0
RC_AA443303_	AA443303	ESTs	10.0
RC_AA446005	AA446005	ESTs	10.0
RC_AA449471	AA449471	ESTs	10.0
RC_AA451877	AA451877	ESTs	10.0

FIGURE 1 (CONT.)

RC_AA478487	AA478487	ESTs 10.0
RC_AA491001_f	AA491001	ESTs Weakly similar to ORF YOR173w 10.0
RC_AA620446	AA620446	ESTs 10.0
RC_AA621131	AA621131	ESTs 10.0
RC_AA621414_	AA621414	Homo sapiens transmembrane protein mRNA 10.0
RC_AA621680	AA621680	Homo sapiens Kruppel-like zinc finger protein 10.0
RC_D25786	D25786	EST 10.0
RC_D56989_f	D56989	ESTs 10.0
RC_D56989_i	D56989	ESTs 10.0
RC_D59420	D59420	EST - RC_D59420 10.0
T87593	T87593	EST - T87593 10.0
U25265	U25265	Human MEK5 mRNA complete cds 10.0
U81787	U81787	Human Wnt10B mRNA complete cds 10.0
W19098	W19098	ESTs 10.0
W26097	W26097	ESTs 10.0
W28390	W28390	Human mRNA for rab GDI alpha complete cds 10.0
W28548	W28548	ESTs 10.0
W28931	W28931	ESTs Weakly similar to D2030.9 [C.elegans] 10.0
W38002_s	W38002	EST - W38002_s 10.0
X04602_s	X04602	Interleukin 6 (B cell stimulatory factor 2) 10.0
X55019_s	X55019	Cholinergic receptor nicotinic delta polypeptide 10.0
RC_AA011576	AA011576	ESTs 10.0
RC_AA015736	AA015736	ESTs Weakly similar to C27H6.5 [C.elegans] 10.0
RC_AA017462	AA017462	ESTs 10.0
RC_AA017547_r	AA017547	ESTs 10.0
RC_AA025061	AA025061	ESTs 10.0
RC_AA037388	AA037388	ESTs 10.0
RC_AA043675	AA043675	EST 10.0
RC_AA047229	AA047229	ESTs Weakly similar to HYPOTHETICAL 41.9 KD 10.0
RC_AA059473	AA059473	ESTs 10.0
RC_AA071193	AA071193	ESTs 10.0
RC_AA075124	AA075124	EST - RC_AA075124 10.0
RC_AA079079	AA079079	EST - RC_AA079079 10.0
RC_AA079120	AA079120	EST - RC_AA079120 10.0
RC_AA083070_	AA083070	EST - RC_AA083070_s 10.0
RC_AA121820	AA121820	ESTs 10.0
RC_AA126583	AA126583	ESTs 10.0

FIGURE 1 (CONT.)

RC_AA131571_	AA131571	ESTs	10.0
RC_AA171426	AA171426	ESTs	10.0
RC_AA219555	AA219555	ESTs	10.0
RC_H05645	H05645	ESTs Weakly similar to R07B7.10 [C.elegans]	10.0
RC_H10761	H10761	ESTs	10.0
RC_H18299	H18299	ESTs	10.0
RC_H51276	H51276	ESTs	10.0
RC_H58934	H58934	ESTs	10.0
RC_H69547	H69547	ESTs Moderately similar to TRANSIENT RECEPTOR POTENTIAL LOCUS C PROTEIN	10.0
RC_N49409	N49409	ESTs Weakly similar to HYPOTHETICAL 46.1 KD	10.0
RC_N62889_s	N62889	ESTs	10.0
RC_N66951	N66951	ESTs	10.0
RC_R00144	R00144	EST - RC_R00144	10.0
RC_R07324	R07324	ESTs	10.0
RC_R16157	R16157	Homo sapiens clone 23770 mRNA sequence	10.0
RC_R33146	R33146	ESTs	10.0
RC_R42333	R42333	ESTs	10.0
RC_R43977	R43977	ESTs Moderately similar to !!!! ALU SUBFAMILY	10.0
RC_R49568	R49568	ESTs	10.0
RC_R66992	R66992	ESTs	10.0
RC_R77302	R77302	ESTs	10.0
RC_T03803	T03803	ESTs	10.0
RC_T51588	T51588	Human mRNA for KIAA0226 gene complete cds	10.0
RC_T58756	T58756	ESTs	10.0
RC_T67285	T67285	EST	10.0
RC_T79768	T79768	ESTs	10.0
RC_T91047	T91047	ESTs	10.0
RC_W04657	W04657	ESTs	10.0
RC_W33178	W33178	ESTs	10.0
RC_W86195	W86195	ESTs Weakly similar to retrovirus-related pol	10.0
RC_Z39319	Z39319	EST	10.0
RC_AA435850	AA435850	ESTs	10.0
RC_AA443800	AA443800	ESTs	10.0
RC_AA456968	AA456968	ESTs	10.0
RC_AA481427	AA481427	ESTs	10.0

FIGURE 1 (CONT.)

		EST	10.0
RC_C21161	C21161	Homo sapiens intermediate conductance calcium-activated potassium channel (hKCa4) mRNA	10.0
RC_D20860	D20860		
RC_H02848_s	H02848	TYROSINE-PROTEIN KINASE RECEPTOR TIE-	10.0
RC_N20468	N20468	ESTs Weakly similar to line-1 protein ORF2	10.0
RC_N39426	N39426	ESTs	10.0
RC_N49285_f	N49285	ESTs	10.0
RC_N50034	N50034	ESTs	10.0
RC_N65972	N65972	ESTs	10.0
RC_N70907	N70907	EST	10.0
RC_T47418	T47418	ESTs	10.0
RC_T48075_f	T48075	Hemoglobin alpha 1	10.0
RC_T52813_s	T52813	Human G0S2 protein gene complete cds	10.0
RC_W38051	W38051	EST - RC_W38051	10.0
RC_W73523	W73523	EST	10.0
RC_AA223746_f	AA223746	MYO-INOSITOL-1(OR 4)-	10.0
RC_AA227849	AA227849	ESTs Weakly similar to RETROVIRUS-RELATED	10.0
RC_AA431337	AA431337	ESTs	10.0
RC_AA447555	AA447555	EST	10.0
RC_AA458945	AA458945	EST	10.0
RC_AA485421_f	AA485421	ESTs	10.0
RC_AA621529_f	AA621529	EST	10.0
RC_H15814_s	H15814	Human apM1 mRNA for GS3109 (novel adipose	10.0
RC_H90310_r	H90310	ESTs Moderately similar to nuclear autoantigen	10.0
RC_N22392	N22392	Homo sapiens oligodendrocyte-specific protein	10.0
RC_N23730_s	N23730	P55-C-FOS PROTO-ONCOGENE PROTEIN	10.0
RC_N50809	N50809	ESTs Highly similar to HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-SPT2 INTERGENIC	10.0
RC_R48732_s	R48732	ESTs	10.0
RC_T47089_s	T47089	Cytochrome P450 subfamily XXI (steroid 21-	10.0
RC_T61256_s	T61256	H.sapiens KHK mRNA for ketohexokinase clone	10.0

FIGURE 1 (CONT.)

RC_T94447_s	T94447	ESTs	10.0
RC_T98199_f	T98199	ESTs	10.0
RC_W72887	W72887	ESTs	10.0
RC_W94688	W94688	Homo sapiens mRNA for perilipin complete cds	10.0
AF000959	AF000959	Homo sapiens transmembrane protein mRNA	5.0
HG2147-	TIGR - HG2147-HT2217	EST - HG2147-HT2217_r	5.0
HG2796-HT2904	TIGR - HG2796-HT2904	EST - HG2796-HT2904	5.0
HG3236-	TIGR - HG3236-HT3413	EST - HG3236-HT3413_f	5.0
HG537-HT537	TIGR - HG537-HT537	EST - HG537-HT537	5.0
L07738	L07738	DIHYDROPRYRIDINE-SENSITIVE L-TYPE	5.0
L10373	L10373	CELL SURFACE GLYCOPROTEIN A15	5.0
L13197	L13197	Pregnancy-associated plasma protein A	5.0
L14927	L14927	Lipocalin 1 (protein migrating faster than albumin	5.0
M57731	M57731	GRO2 oncogene	5.0
M62402	M62402	Insulin-like growth factor binding protein 6	5.0
M72885_mal	M72885	Human G0S2 protein gene complete cds	5.0
S68874	S68874	Prostaglandin E receptor 3 (subtype EP3)	5.0
U32674	U32674	EST - U32674	5.0
U60115	U60115	Homo sapiens skeletal muscle LIM-protein FHL1	5.0
U92457	U92457	Glutamate receptor metabotropic 4	5.0
X03350	X03350	Alcohol dehydrogenase 2 (class I) beta polypeptide	5.0
X98085	X98085	Tenascin R (restrictin janusin)	5.0
Z84721_cds2	Z84721	Hemoglobin alpha 1	5.0
AA044622	AA044622	ESTs Weakly similar to ZINC FINGER PROTEIN	5.0
AA059327_r	AA059327	Homo sapiens clone 23718 mRNA sequence	5.0
AA062932	AA062932	Homo sapiens mRNA for GNAS1 protein (IMAGE	5.0
AA082561_s	AA082561	EST - AA082561_s	5.0
AA093348	AA093348	Homo sapiens secreted frizzled related protein	5.0
AA166651	AA166651	ESTs Weakly similar to HYPOTHETICAL 39.7 KD	5.0
AA191072	AA191072	EST - AA191072	5.0

FIGURE 1 (CONT.)

AA210757	AA210757	Transcription factor 3 (E2A immunoglobulin	5.0
AA232121_r	AA232121	Human tyrosyl-tRNA synthetase mRNA complete	5.0
AA247434	AA247434	ESTs Highly similar to OVARIAN GRANULOSA	5.0
AA252752	AA252752	ESTs	5.0
AA278194	AA278194	Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene an unknown putative gene a	5.0
AA291786_s	AA291786	ESTs Weakly similar to HYPOTHETICAL	5.0
AA400044	AA400044	Human clone 23803 mRNA partial cds	5.0
AA402109	AA402109	ESTs	5.0
AA402971_s	AA402971	ESTs Moderately similar to serine protease	5.0
AA416829	AA416829	ESTs	5.0
AA418214	AA418214	ESTs Weakly similar to APK1 antigen [H.sapiens]	5.0
AA422123_i	AA422123	ESTs Weakly similar to eukaryotic initiation factor	5.0
AA448946_r	AA448946	ESTs	5.0
AA461426_r	AA461426	ESTs	5.0
AB002361	AB002361	Human mRNA for KIAA0363 gene partial cds	5.0
AF001900	AF001900	Homo sapiens secreted frizzled related protein	5.0
C16161_s	C16161	ESTs	5.0
C17282	C17282	ESTs Weakly similar to L8083.1 gene product	5.0
D10216_s	D10216	POU domain class 1 transcription factor 1 (Pit1	5.0
D31381	D31381	ESTs Weakly similar to cytoplasmic dynein light	5.0
D88213	D88213	Amine oxidase copper containing 2 (retina-specific)	5.0
F15201	F15201	EST - F15201	5.0
H30778	H30778	ESTs	5.0
L34155	L34155	Laminin alpha 3 (nicein (150kD) kalinin (165kD)	5.0
N39361	N39361	ESTs Highly similar to GLYCINE-RICH	5.0
N40774	N40774	ESTs	5.0

FIGURE 1 (CONT.)

N99542	N99542	EST 5.0
R19997	R19997	Homo sapiens exportin t mRNA complete cds 5.0
R24011	R24011	ESTs 5.0
R25944_f	R25944	ESTs Moderately similar to !!!! ALU SUBFAMILY 5.0
R68735	R68735	H.sapiens mRNA for phosphoinositide 3-kinase 5.0
R81474	R81474	ESTs 5.0
R88038	R88038	Acyl-Coenzyme A dehydrogenase very long chain 5.0
RC_AA007153	AA007153	ESTs 5.0
RC_AA019031	AA019031	ESTs 5.0
RC_AA025351	AA025351	ESTs 5.0
RC_AA033874	AA033874	ESTs 5.0
RC_AA046747	AA046747	ESTs 5.0
RC_AA126429	AA126429	ESTs Highly similar to LIGATIN [H.sapiens] 5.0
RC_AA151872	AA151872	ESTs 5.0
RC_AA215643	AA215643	ESTs 5.0
RC_AA402268	AA402268	Homo sapiens mRNA for KIAA0652 protein 5.0
RC_AA402613	AA402613	ESTs 5.0
RC_AA405449	AA405449	ESTs 5.0
RC_AA422146	AA422146	ESTs 5.0
RC_AA427627	AA427627	ESTs Weakly similar to potassium-dependent 5.0
RC_AA446027_	AA446027	Early growth response 2 (Krox-20 (Drosophila) 5.0
RC_AA459944	AA459944	ESTs 5.0
RC_AA463929	AA463929	ESTs 5.0
RC_AA478305	AA478305	Homo sapiens chromosome 19 cosmid R27216 5.0
RC_AA482546_	AA482546	Human mRNA for KIAA0124 gene partial cds 5.0
RC_AA485409	AA485409	ESTs 5.0
RC_AA487576	AA487576	ESTs 5.0
RC_AA489499	AA489499	ESTs 5.0
RC_AA496980	AA496980	ESTs 5.0
RC_AA521454	AA521454	ESTs 5.0
RC_AA608802	AA608802	ESTs 5.0
RC_AA609785	AA609785	ESTs 5.0
RC_AA621430	AA621430	Homo sapiens mRNA for doublecortin 5.0
U15637_s	U15637	Human LMP1 associated protein mRNA complete 5.0
U51704	U51704	ESTs 5.0
U73394_f	U73394	Homo sapiens killer cell receptor (KIR103) mRNA 5.0

FIGURE 1 (CONT.)

U76456	U76456	Human tissue inhibitor of metalloproteinase 4	5.0
U83171	U83171	Human macrophage-derived chemokine precursor	5.0
W26652	W26652	ESTs	5.0
W29012	W29012	ESTs	5.0
W37319	W37319	ESTs	5.0
W37398	W37398	ESTs	5.0
W44533	W44533	MAP KINASE PHOSPHATASE-1	5.0
X72308	X72308	MONOCYTE CHEMOTACTIC PROTEIN 3	5.0
RC_AA025837	AA025837	ESTs	5.0
RC_AA029927_i	AA029927	ESTs	5.0
RC_AA045306	AA045306	ESTs	5.0
RC_AA063174	AA063174	ESTs	5.0
RC_AA070500	AA070500	EST - RC_AA070500	5.0
RC_AA074885	AA074885	Homo sapiens macrophage receptor MARCO	5.0
RC_AA099820	AA099820	ESTs	5.0
RC_AA113289	AA113289	EST - RC_AA113289	5.0
RC_AA207059	AA207059	ESTs Moderately similar to !!!! ALU SUBFAMILY	5.0
RC_F01449_f	F01449	ESTs	5.0
RC_H41280	H41280	ESTs	5.0
RC_H52172	H52172	EST - RC_H52172	5.0
RC_H58222	H58222	ESTs	5.0
RC_N52176	N52176	ESTs	5.0
RC_N66616	N66616	ESTs	5.0
RC_N67583	N67583	ESTs Moderately similar to CMRF35 ANTIGEN	5.0
RC_N73988	N73988	ESTs Weakly similar to No definition line found	5.0
RC_N92239	N92239	ESTs Highly similar to LATENT TRANSFORMING GROWTH FACTOR BETA	5.0
RC_R26065	R26065	ESTs	5.0
RC_R43035	R43035	ESTs	5.0
RC_R51898	R51898	ESTs	5.0
RC_R84968	R84968	ESTs	5.0
RC_R96306	R96306	ESTs	5.0
RC_R98491	R98491	ESTs	5.0
RC_T10142	T10142	ESTs	5.0

FIGURE 1 (CONT.)

RC_T54659	T54659	EST	5.0
RC_T57857	T57857	ESTs	5.0
RC_T86674	T86674	ESTs	5.0
RC_T89160_f	T89160	ESTs	5.0
RC_T91185	T91185	ESTs	5.0
RC_Z39975	Z39975	ESTs	5.0
RC_Z41480	Z41480	ESTs	5.0
RC_AA020736	AA020736	EST - RC_AA020736	5.0
RC_AA034378_f	AA034378	ESTs	5.0
RC_AA065096	AA065096	EST - RC_AA065096	5.0
RC_AA084362_f	AA084362	EST - RC_AA084362_f	5.0
RC_AA234826	AA234826	EST	5.0
RC_AA234895	AA234895	ESTs	5.0
RC_AA236534	AA236534	ESTs	5.0
RC_AA405791	AA405791	ESTs	5.0
RC_AA406050	AA406050	Homo sapiens Tax interaction protein 33 mRNA	5.0
RC_AA412707	AA412707	ESTs	5.0
RC_AA428964	AA428964	Homo sapiens serine protease-like protease (nes1)	5.0
RC_AA463902	AA463902	ESTs	5.0
RC_AA485080	AA485080	ESTs	5.0
RC_AA488839	AA488839	ESTs	5.0
RC_F04052	F04052	Homo sapiens clone 23763 unknown mRNA partial	5.0
RC_F10528_f	F10528	ESTs Moderately similar to !!!! ALU CLASS B	5.0
RC_H90434	H90434	EST	5.0
RC_H95958	H95958	ESTs	5.0
RC_H97387_s	H97387	ESTs	5.0
RC_N23399	N23399	ESTs	5.0
RC_N35978	N35978	ESTs	5.0
RC_N50937	N50937	EST	5.0
RC_N59860_s	N59860	Human clone 23947 mRNA partial cds	5.0
RC_N69476	N69476	ESTs	5.0
RC_N90744	N90744	ESTs	5.0
RC_R95132	R95132	EST - RC_R95132	5.0
RC_T41144_s	T41144	ESTs	5.0
RC_T77892	T77892	EST - RC_T77892	5.0
RC_T81824	T81824	EST	5.0
RC_W74257	W74257	EST - RC_W74257	5.0

FIGURE 1 (CONT.)

RC_W78168	W78168	ESTs	5.0
RC_W86214	W86214	ESTs	5.0
RC_W87535	W87535	ESTs	5.0
RC_AA297532_f	AA297532	ESTs	5.0
RC_AA299629	AA299629	RNA-BINDING PROTEIN FUS/TLS	5.0
RC_AA383038	AA383038	EST	5.0
RC_AA398531	AA398531	ESTs	5.0
RC_AA401695	AA401695	EST	5.0
RC_AA402933	AA402933	ESTs	5.0
RC_AA405763	AA405763	ESTs	5.0
RC_AA421483	AA421483	EST	5.0
RC_AA435746_f	AA435746	Homo sapiens mRNA for KIAA0538 protein partial	5.0
RC_AA456975_	AA456975	Apolipoprotein D	5.0
RC_AA459658	AA459658	ESTs	5.0
RC_AA609122	AA609122	EST	5.0
RC_AA609214	AA609214	ESTs Weakly similar to ADAM 20 [H.sapiens]	5.0
RC_F04387_s	F04387	AXL receptor tyrosine kinase	5.0
RC_H59063	H59063	EST - RC_H59063	5.0
RC_H79007_f	H79007	ESTs	5.0
RC_H83465_f	H83465	EST - RC_H83465_f	5.0
RC_N27118	N27118	ESTs Highly similar to HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN	5.0
RC_N56898_s	N56898	Glutathione S-transferase M5	5.0
RC_R01398	R01398	EST - RC_R01398	5.0
RC_R44214_r	R44214	ESTs	5.0
RC_R71403_f	R71403	ESTs	5.0
RC_T61561_s	T61561	VON WILLEBRAND FACTOR PRECURSOR	5.0
RC_T94357_f	T94357	ESTs	5.0
RC_W61260	W61260	ESTs	5.0
RC_W87480	W87480	Homo sapiens STAT-induced STAT inhibitor-2	5.0
RC_T55547	T55547	ESTs	3.3
RC_W44733	W44733	ESTs	3.3
RC_AA401564	AA401564	ESTs	3.3
RC_N34417	N34417	ESTs	3.3
RC_N53145_f	N53145	EST - RC_N53145_f	3.3
RC_N81130	N81130	ESTs	3.3
RC_R02384	R02384	Pregnancy-specific beta-1 glycoprotein 6	3.3
RC_W73194	W73194	ESTs	3.3

FIGURE 1 (CONT.)

Tetranectin (plasminogen-binding protein)	3.3	RC_W73889_s W73889
ESTs	3.3	RC_W92278 W92278
ESTs	3.3	RC_R48540_s R48540
EST - YEL024w/RIP1	3.3	YEL024w/RIP1

FIGURE 2

Affymetrix ID	Accession	Gene Name	Ratio breast v. tumor
RC_AA025277	AA025277	ESTs	10.0
RC_H49425	H49425	ESTs	10.0
RC_N51657	N51657	EST	10.0
RC_R16733	R16733	ESTs	10.0
RC_AA079072_s	AA079072	Insulin-like growth factor binding protein	10.0
HG1428-HT1428	TIGR - HG1428-	EST - HG1428-HT1428	10.0
L49169	L49169	Human G0S3 mRNA complete cds	10.0
X51441	X51441	SERUM AMYLOID A PROTEIN	10.0
M84526	M84526	D component of complement (adipsin)	10.0
R69417	R69417	ESTs	10.0
RC_AA621680	AA621680	Homo sapiens Kruppel-like zinc finger	10.0
RC_AA071193	AA071193	ESTs	10.0
RC_N66951	N66951	ESTs	10.0
RC_R33146	R33146	ESTs	10.0
RC_N23730_s	N23730	P55-C-FOS PROTO-ONCOGENE	10.0
RC_W94688	W94688	Homo sapiens mRNA for perilipin	10.0
HG2157-HT2227	TIGR - HG2157-	EST - HG2157-HT2227	10.0
HG2841-HT2969	TIGR - HG2841-	EST - HG2841-HT2969	10.0
J02874	J02874	Fatty acid binding protein 4 adipocyte	10.0
J03474	J03474	SERUM AMYLOID A PROTEIN	10.0
L19871	L19871	Activating transcription factor 3	10.0
M12963	M12963	Alcohol dehydrogenase 1 (class I) alpha	10.0
M21305	M21305	EST - M21305	10.0
M22430	M22430	Phospholipase A2 group IIA (platelets	10.0
M25079	M25079	Hemoglobin beta	10.0
M27826	M27826	Human endogenous retroviral protease	10.0
M30185	M30185	Cholesteryl ester transfer protein plasma	10.0
U22961	U22961	EST - U22961	10.0
U48251	U48251	Homo sapiens protein kinase C-binding	10.0
U88902_cds1_f	U88902	EST - U88902_cds1_f	10.0
X00129	X00129	PLASMA RETINOL-BINDING	10.0
X04602	X04602	Interleukin 6 (B cell stimulatory factor 2)	10.0
X64559	X64559	Tetranectin (plasminogen-binding	10.0
X75958	X75958	TrkB {alternatively spliced} [human	10.0
X87344_cds10_r	X87344	H.sapiens DMA DMB HLA-Z1 IPP2	10.0
X99142	X99142	H.sapiens mRNA for hHKb1 protein	10.0
Z49269	Z49269	Homo sapiens MIP-1 delta mRNA	10.0
AA081995	AA081995	EST - AA081995	10.0
AA090439	AA090439	ESTs	10.0

FIGURE 2 (CONT.)

AA137107	AA137107	ESTs	10.0
AA203296	AA203296	ESTs	10.0
AA285284	AA285284	ESTs Highly similar to ISOCITRATE	10.0
AA310850	AA310850	ESTs	10.0
AA418143	AA418143	ESTs	10.0
AA425719	AA425719	ESTs	10.0
AA427379	AA427379	ESTs	10.0
AA452705	AA452705	ESTs Weakly similar to D2045.9	10.0
AB002328	AB002328	Human mRNA for KIAA0330 gene	10.0
AF000575_s	AF000575	Homo sapiens clone 17.11	10.0
M12272_s	M12272	Alcohol dehydrogenase 3 (class I) gamma	10.0
M26315_cds2_s	M26315	CD8 antigen alpha polypeptide (p32)	10.0
M64936_i	M64936	Homo sapiens retinoic acid-inducible	10.0
M81349	M81349	SERUM AMYLOID A-4 PROTEIN	10.0
N73185	N73185	EST	10.0
N79674_s	N79674	ESTs	10.0
N88827	N88827	ESTs	10.0
N91071_s	N91071	ESTs	10.0
R21149	R21149	ESTs Highly similar to RAB GDP	10.0
RC_AA009764	AA009764	ESTs	10.0
RC_AA017254	AA017254	ESTs	10.0
RC_AA019300	AA019300	ESTs	10.0
RC_AA026280	AA026280	ESTs	10.0
RC_AA115253	AA115253	ESTs	10.0
RC_AA128617	AA128617	ESTs	10.0
RC_AA179338	AA179338	ESTs	10.0
RC_AA223237	AA223237	ESTs Moderately similar to retrovirus-	10.0
RC_AA234308	AA234308	ESTs	10.0
RC_AA251772	AA251772	H.sapiens mRNA for HES1 protein	10.0
RC_AA279673	AA279673	Homo sapiens mRNA for HsGAK	10.0
RC_AA411443	AA411443	ESTs	10.0
RC_AA416947	AA416947	ESTs	10.0
RC_AA426584	AA426584	ESTs	10.0
RC_AA434113	AA434113	ESTs	10.0
RC_AA443303_s	AA443303	ESTs	10.0
RC_AA446005	AA446005	ESTs	10.0
RC_AA449471	AA449471	ESTs	10.0
RC_AA451877	AA451877	ESTs	10.0
RC_AA478487	AA478487	ESTs	10.0
RC_AA491001_f	AA491001	ESTs Weakly similar to ORF YOR173w	10.0

FIGURE 2 (CONT.)

RC_AA620446	AA620446	ESTs	10.0
RC_AA621131	AA621131	ESTs	10.0
RC_AA621414_s	AA621414	Homo sapiens transmembrane protein	10.0
RC_D25786	D25786	EST	10.0
RC_D56989_f	D56989	ESTs	10.0
RC_D56989_i	D56989	ESTs	10.0
RC_D59420	D59420	EST - RC_D59420	10.0
T87593	T87593	EST - T87593	10.0
U25265	U25265	Human MEK5 mRNA complete cds	10.0
U81787	U81787	Human Wnt10B mRNA complete cds	10.0
W19098	W19098	ESTs	10.0
W26097	W26097	ESTs	10.0
W28390	W28390	Human mRNA for rab GDI alpha	10.0
W28548	W28548	ESTs	10.0
W28931	W28931	ESTs Weakly similar to D2030.9	10.0
AF001900	AF001900	Homo sapiens secreted frizzled related	5.0
RC_AA402268	AA402268	Homo sapiens mRNA for KIAA0652	5.0
RC_AA608802	AA608802	ESTs	5.0
RC_F01449_f	F01449	ESTs	5.0
RC_AA034378_f	AA034378	ESTs	5.0
RC_AA456975_s	AA456975	Apolipoprotein D	5.0

FIGURE 3

Affymetrix ID	Accession	Gene Name	ratio breast vs tumor
RC_AA079072_s	AA079072	Insulin-like growth factor binding protein 6	10.0
L49169	L49169	Human G0S3 mRNA complete cds	10.0
X51441	X51441	SERUM AMYLOID A PROTEIN PRECURSOR	10.0
RC_N66951	N66951	ESTs	10.0
RC_R33146	R33146	ESTs	10.0
M30185	M30185	Cholesteryl ester transfer protein plasma	10.0
U22961	U22961	EST - U22961	10.0
X64559	X64559	Tetranectin (plasminogen-binding protein)	10.0
Z49269	Z49269	Homo sapiens MIP-1 delta mRNA complete cds	10.0
AA427379	AA427379	ESTs	10.0

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FIGURE 4

Affymetrix ID	Acession	Gene Name	Ratio tumor v. breast
RC_T79956	T79956	ESTs	135.3
RC_AA453640	AA453640	ESTs	121.4
RC_AA453638	AA453638	EST - RC_AA453638	107.3
RC_AA461322	AA461322	EST	81.8
RC_AA461510	AA461510	EST - RC_AA461510	75.3
RC_R67275_s	R67275	Collagen type XI alpha 1	72.9
RC_AA453518	AA453518	ESTs	61.5
RC_N27351	N27351	EST - RC_N27351	57.1
RC_AA486737	AA486737	H.sapiens mRNA for Sm protein F	53.9
RC_AA453479	AA453479	Human focal adhesion kinase (FAK) mRNA complete cds	53.2
RC_AA285050	AA285050	ESTs Weakly similar to zinc-finger protein Zn72D	52.0
RC_AA291468	AA291468	ESTs	46.8
RC_Z40805	Z40805	ESTs	45.7
RC_AA169440	AA169440	ESTs	38.9
D90041_s	D90041	ARYLAMINE N-ACETYLTRANSFERASE	33.6
RC_AA621202	AA621202	ESTs	33.5
RC_AA232294	AA232294	EST - RC_AA232294	32.6
RC_R86839	R86839	EST - RC_R86839	32.4
S70585_mal	S70585	GLYCOPROTEIN HORMONES ALPHA CHAIN	31.3
RC_AA453641	AA453641	EST	31.1
RC_AA609955	AA609955	EST	30.6
RC_AA283905	AA283905	ESTs	28.3
RC_AA211831	AA211831	EST - RC_AA211831	28.1
RC_AA412090	AA412090	ESTs	28.0
RC_N27159_s	N27159	Inhibin beta A (activin A activin AB alpha polypeptide)	25.5
RC_AA421289	AA421289	ESTs Weakly similar to ZINC FINGER PROTEIN MFG1	25.5
RC_T16687	T16687	ESTs	25.1
RC_R65763	R65763	EST	23.9
RC_AA487987	AA487987	EST	23.8
RC_H99309	H99309	Human TFIID subunits TAF20 and TAF15 mRNA	23.6
RC_R97063	R97063	ESTs	22.8
RC_AA232940	AA232940	EST - RC_AA232940	21.7
RC_AA463189	AA463189	ESTs	20.9
RC_AA421171	AA421171	ESTs	19.5
RC_AA251875	AA251875	ESTs Moderately similar to POL POLYPROTEIN [Feline	19.4
RC_AA054228	AA054228	ESTs	17.7
RC_D51215_f	D51215	EST - RC_D51215_f	17.4
RC_AA621462	AA621462	CARCINOEMBRYONIC ANTIGEN PRECURSOR	17.1
RC_AA505133	AA505133	ESTs	17.1

FIGURE 4 (CONT.)

RC_AA232508	AA232508	ESTs	17.0
RC_AA024659	AA024659	H.sapiens mRNA for hHKb1 protein	16.9
RC_AA488191	AA488191	ESTs	16.8
RC_AA211158	AA211158	EST - RC_AA211158	16.8
RC_AA290674	AA290674	Human 4E-binding protein 1 mRNA complete cds	16.3
RC_AA481883	AA481883	ESTs	16.2
RC_AA196768	AA196768	ESTs	16.1
H83527_s	H83527	ESTs Highly similar to thyroid disease hypothetical	16.1
RC_AA196721	AA196721	EST - RC_AA196721	16.1
RC_D51172	D51172	ESTs	15.9
RC_T25875	T25875	Homo sapiens clone 23967 unknown mRNA partial cds	15.8
X57579	X57579	Inhibin beta A (activin A activin AB alpha polypeptide)	15.8
J05068	J05068	TRANSCOBALAMIN I PRECURSOR	15.7
RC_AA487233	AA487233	ESTs Moderately similar to !!!! ALU SUBFAMILY SP	15.6
RC_AA479969	AA479969	ESTs	15.4
RC_AA191404	AA191404	ESTs	15.2
RC_AA262969	AA262969	ESTs Weakly similar to B0334.4 [C.elegans]	14.9
RC_AA436611	AA436611	Human fibroblast activation protein mRNA complete cds	14.7
RC_R51309	R51309	ESTs	14.6
RC_AA461297	AA461297	ESTs	14.6
RC_AA250843	AA250843	Interferon regulatory factor 5	14.6
RC_AA430032	AA430032	ESTs Moderately similar to PTTG gene product	14.4
RC_AA280679	AA280679	ESTs	14.4
RC_AA412029	AA412029	ESTs	14.4
M81057	M81057	Carboxypeptidase B1 (tissue)	14.4
RC_R07976	R07976	ESTs Highly similar to HYPOTHETICAL 21.5 KD	14.3
U75285_ma1	U75285	Human effector cell protease receptor-1 (EPR-1) gene	14.3
RC_R46627	R46627	ESTs	14.2
RC_AA461559	AA461559	Chromogranin A (parathyroid secretory protein 1)	14.1
AA092129_f	AA092129	ESTs Moderately similar to 25E8.1 [D.melanogaster]	14.0
RC_AA436893	AA436893	ESTs Weakly similar to TH1 protein [D.melanogaster]	14.0
M23263	M23263	Androgen receptor (dihydrotestosterone receptor testicular	13.9
RC_AA465345	AA465345	ESTs	13.9
RC_AA486538	AA486538	ESTs Weakly similar to hypothetical protein 1 [H.sapiens]	13.9
RC_D20379	D20379	ESTs	13.7
RC_AA076138	AA076138	Homo sapiens histone macroH2A1.2 mRNA complete cds	13.5
RC_W60486	W60486	ESTs Moderately similar to T11G6.8 [C.elegans]	13.5
RC_AA045074	AA045074	ESTs Weakly similar to 52-kD SS-A/Ro autoantigen	13.4
RC_AA032243	AA032243	EST - RC_AA032243	13.4
RC_F01444_f	F01444	Homo sapiens KIAA0440 mRNA partial cds	13.4

FIGURE 4 (CONT.)

AA401334	AA401334	ESTs	13.3
RC_T78922_s	T78922	Homo sapiens mRNA for SCGF-beta complete cds	13.3
RC_D60354_s	D60354	Human mRNA for KIAA0007 gene partial cds	13.3
RC_AA431350	AA431350	ESTs Moderately similar to !!!! ALU SUBFAMILY SC	13.1
RC_AA412065	AA412065	EST - RC_AA412065	13.1
RC_AA406635	AA406635	ESTs	13.1
RC_AA431738	AA431738	EST	13.1
RC_R61740_f	R61740	Homo sapiens regulator of G-protein signalling 12	13.0
RC_R54950	R54950	ESTs	12.8
RC_AA405488	AA405488	ESTs	12.7
RC_AA418749	AA418749	EST	12.7
AA037285	AA037285	Homo sapiens mRNA for A+U-rich element RNA binding	12.5
RC_AA233796	AA233796	ESTs	12.5
RC_AA219305	AA219305	EST	12.4
RC_AA252245	AA252245	ESTs	12.4
RC_AA041276	AA041276	ESTs Weakly similar to !!!! ALU SUBFAMILY SX	12.3
RC_AA463874	AA463874	Homo sapiens ES/130 mRNA complete cds	12.3
RC_AA461528	AA461528	ESTs	12.2
RC_AA099404	AA099404	ESTs	12.2
RC_AA443985	AA443985	ESTs	12.2
RC_AA214305	AA214305	ESTs	12.1
AA220223	AA220223	Fibroblast growth factor receptor 2 (bacteria-expressed	12.1
RC_AA478571	AA478571	Glutamine-fructose-6-phosphate transaminase	12.1
U31875	U31875	Human Hep27 protein mRNA complete cds	12.1
RC_AA253217	AA253217	ESTs	11.8
RC_AA470074	AA470074	ESTs	11.5
RC_AA236010	AA236010	ESTs	11.4
J03589	J03589	UBIQUITIN-LIKE PROTEIN GDX	11.4
D82307	D82307	ESTs Weakly similar to TH1 protein [D.melanogaster]	11.4
RC_AA430002	AA430002	ESTs	11.4
RC_R22952_s	R22952	ESTs	11.3
RC_AA179298	AA179298	Homo sapiens chromosome 9 P1 clone 11659	11.3
RC_W56363	W56363	ESTs Weakly similar to extracellular protein [H.sapiens]	11.3
RC_AA449232	AA449232	EST	11.2
RC_AA444054	AA444054	ESTs Weakly similar to transmembrane protein [H.sapiens]	11.1
RC_AA281733	AA281733	ESTs	11.0
RC_AA452601	AA452601	EST	11.0
RC_AA035630	AA035630	Homo sapiens U4/U6 small nuclear ribonucleoprotein	10.9
RC_AA235117	AA235117	ESTs Weakly similar to espin [R.norvegicus]	10.9
RC_AA279418	AA279418	ESTs	10.9

FIGURE 4 (CONT.)

RC_AA432069	AA432069	ESTs	10.8
RC_AA453630	AA453630	EST	10.7
RC_W44657	W44657	EST	10.7
RC_R40431	R40431	ESTs	10.6
RC_AA405098	AA405098	ESTs Weakly similar to MOESIN/EZRIN/RADIXIN	10.6
RC_AA411425	AA411425	ESTs	10.5
RC_AA423956	AA423956	ESTs	10.5
RC_AA599259	AA599259	Human splicesomal protein (SAP 61) mRNA complete cds	10.4
X62078	X62078	GANGLIOSIDE GM2 ACTIVATOR PRECURSOR	10.4
RC_AA253170	AA253170	EST	10.4
RC_AA459347	AA459347	ESTs	10.4
RC_AA251430	AA251430	ESTs Highly similar to RAS-RELATED PROTEIN RAB-	10.3
RC_AA470156	AA470156	ESTs Weakly similar to dynein 74K chain cytosolic	10.3
RC_T64933_f	T64933	ESTs	10.3
RC_AA281290	AA281290	ESTs Highly similar to ZINC FINGER PROTEIN 85	10.2
RC_AA280609	AA280609	ESTs Weakly similar to K02B2.3 gene product [C.elegans]	10.2
RC_AA449832	AA449832	ESTs	10.1
RC_AA427898	AA427898	ESTs Weakly similar to trabecular meshwork inducible	10.0
RC_AA609867	AA609867	ESTs Weakly similar to No definition line found	10.0
RC_R49198_i	R49198	H.sapiens DAP-3 mRNA	9.9
RC_AA465158	AA465158	EST	9.9
RC_AA112396	AA112396	ESTs	9.8
RC_AA207015	AA207015	ESTs	9.8
RC_R06986_f	R06986	ESTs	9.7
M34338	M34338	Spermidine synthase	9.7
RC_AA228030	AA228030	ESTs	9.7
RC_AA447982	AA447982	ESTs Weakly similar to R01H10.6 [C.elegans]	9.7
Z14982_ma1	Z14982	PROTEASOME COMPONENT C13 PRECURSOR	9.7
RC_AA176247	AA176247	EST	9.6
RC_T97341	T97341	EST - RC_T97341	9.6
W26392	W26392	ESTs Highly similar to OVOSTATIN PRECURSOR	9.6
RC_AA143190	AA143190	ESTs Highly similar to HYPOTHETICAL 23.1 KD	9.5
RC_AA452578	AA452578	ESTs	9.5
RC_W92713	W92713	ESTs	9.4
RC_AA282914	AA282914	ESTs	9.4
RC_AA461476	AA461476	ESTs Highly similar to PUTATIVE ATP-DEPENDENT	9.4
RC_AA258057	AA258057	ESTs	9.4
RC_W87751	W87751	ESTs	9.4
RC_N21678	N21678	ESTs	9.3
RC_AA262111	AA262111	ESTs	9.3

FIGURE 4 (CONT.)

RC_AA490929	AA490929	EST	9.3
RC_N70690	N70690	ESTs	9.3
RC_N80716	N80716	ESTs	9.3
RC_AA007344	AA007344	ESTs	9.2
RC_W73140	W73140	ESTs Highly similar to TRYPSINOGEN ANIONIC	9.2
RC_D14657	D14657	Human mRNA for KIAA0101 gene complete cds	9.2
RC_T16308_f	T16308	ESTs	9.1
RC_AA447666	AA447666	Human CENP-F kinetochore protein mRNA complete cds	9.1
RC_AA243020	AA243020	H.sapiens mRNA for disintegrin-metalloprotease (partial)	9.1
RC_AA431478	AA431478	ESTs	9.1
RC_R38919_i	R38919	EST	9.0
RC_R60223_s	R60223	ESTs	9.0
RC_R70379_s	R70379	Human germline IgD chain gene C-region C-delta-1	9.0
HG2981-	TIGR - HG2981-	EST - HG2981-HT3127	9.0
M86757	M86757	S100 calcium-binding protein A7 (psoriasin 1)	8.9
X72755	X72755	H.sapiens Humig mRNA	8.8
RC_AA347209	AA347209	Human mRNA for KIAA0324 gene partial cds	8.8
RC_AA485041	AA485041	ESTs	8.8
RC_AA443342	AA443342	ESTs	8.7
RC_AA481281	AA481281	ESTs	8.7
RC_T96361_s	T96361	MULTIFUNCTIONAL AMINOACYL-TRNA	8.7
RC_H18027_s	H18027	Homo sapiens clone 23785 mRNA sequence	8.6
RC_AA608723	AA608723	ESTs	8.6
M86752	M86752	TRANSFORMATION-SENSITIVE PROTEIN IEF SSP	8.6
RC_AA457018	AA457018	ESTs	8.5
RC_AA113011	AA113011	Human mRNA for KIAA0314 gene partial cds	8.5
RC_H96237_s	H96237	Collagen type XI alpha 1	8.5
RC_AA024835	AA024835	Homo sapiens Shab-related delayed-rectifier K+ channel	8.4
S85655	S85655	Prohibitin	8.4
RC_N99976	N99976	ESTs	8.4
RC_T65004	T65004	EST - RC_T65004	8.4
RC_N93197	N93197	ESTs	8.3
RC_H72948_s	H72948	ESTs Highly similar to BONE/CARTILAGE	8.3
RC_AA489510	AA489510	Homo sapiens clone 23716 mRNA sequence	8.3
RC_Z39971_s	Z39971	ESTs	8.3
RC_AA236037	AA236037	ESTs Highly similar to HYPOTHETICAL 37.8 KD	8.2
J05070	J05070	Matrix metalloproteinase 2 (gelatinase A collagenase type	8.2
RC_H98621_s	H98621	Homo sapiens mRNA for KIAA0617 protein complete cds	8.1
RC_R40177	R40177	ESTs	8.1
RC_D60302	D60302	ESTs	8.1

FIGURE 4 (CONT.)

RC_AA419225	AA419225	Human mariner-like element-containing mRNA clone	8.1
RC_W93659	W93659	ESTs	8.0
RC_AA233545	AA233545	ESTs Weakly similar to HYPOTHETICAL 26.1 KD	8.0
RC_N39415	N39415	ESTs Highly similar to OSTEOINDUCTIVE FACTOR	8.0
RC_AA436370	AA436370	ESTs Highly similar to ADP-RIBOSYLATION FACTOR-RAP1 GTPase activating protein 1	8.0
RC_F01538_s	F01538	ESTs	7.9
RC_AA053319	AA053319	ESTs	7.9
RC_N69464	N69464	ESTs Weakly similar to LINE-1 REVERSE	7.9
RC_AA458882	AA458882	Replication protein A (E coli RecA homolog RAD51	7.9
RC_N33011_s	N33011	EST	7.9
RC_AA421750	AA421750	ESTs	7.9
RC_AA235009	AA235009	ESTs	7.9
RC_AA447574	AA447574	ESTs	7.9
RC_R01634	R01634	ESTs	7.9
RC_R47948_i	R47948	EST - RC_N53950	7.9
RC_N53950	N53950	ESTs Weakly similar to HYPOTHETICAL 88.1 KD	7.8
RC_AA150182	AA150182	Homo sapiens Ran binding protein 2 (RanBP2alpha)	7.8
RC_AA446486	AA446486	EST - RC_AA342084	7.8
RC_AA342084	AA342084	ESTs	7.8
RC_AA417213	AA417213	EST	7.8
RC_AA609170	AA609170	EST - RC_N46435	7.8
RC_N46435	N46435	Human mRNA for KIAA0136 gene partial cds	7.8
RC_N54916	N54916	ESTs	7.7
RC_T88814	T88814	Homo sapiens mRNA for tyrosyl sulfotransferase-2	7.7
RC_AA459389	AA459389	ESTs	7.7
RC_AA463693	AA463693	ESTs Highly similar to EPIDERMAL GROWTH	7.6
RC_H99879	H99879	Human melanoma antigen p15 mRNA complete cds	7.6
U19796	U19796	ESTs	7.6
RC_T68871	T68871	EST	7.6
RC_AA446008	AA446008	Homo sapiens clone 24703 beta-tubulin mRNA complete	7.6
RC_T03306	T03306	EST - HG2981-HT3938	7.6
HG2981-	TIGR - HG2981-	ESTs	7.5
RC_N67119	N67119	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	7.5
RC_AA442767	AA442767	Human mRNA for KIAA0170 gene complete cds	7.5
RC_AA454566	AA454566	ESTs	7.5
RC_AA476937	AA476937	EST - W01296	7.5
W01296	W01296	ESTs	7.5
RC_AA282074	AA282074	Calcineurin B	7.5
AA094752	AA094752	Homo sapiens mRNA for osteoblast specific factor 2 (OSF-	7.5
D13666	D13666		

FIGURE 4 (CONT.)

RC_N67889	N67889	ESTs	7.4
RC_AA609309	AA609309	ESTs	7.4
RC_AA412477	AA412477	EST	7.4
RC_AA459392	AA459392	ESTs	7.4
RC_AA599042	AA599042	EST	7.4
RC_W73520	W73520	ESTs Highly similar to HYPOTHETICAL 28.5 KD	7.4
RC_AA069476	AA069476	H.sapiens mRNA for surface glycoprotein	7.4
RC_AA287061	AA287061	ESTs	7.4
RC_AA411952	AA411952	Homo sapiens mRNA for GalT4 protein	7.4
RC_AA410190	AA410190	ESTs	7.4
RC_AA486256	AA486256	ESTs Moderately similar to breast cancer suppressor	7.4
X02530	X02530	Interferon (gamma)-induced cell line protein 10 from	7.4
RC_D59489	D59489	ESTs	7.4
RC_AA283006	AA283006	ESTs Highly similar to CHROMOSOME	7.3
RC_AA443794	AA443794	ESTs	7.3
RC_F13642	F13642	ESTs	7.3
RC_AA426372	AA426372	Human mRNA for histone H1x complete cds	7.3
RC_AA446869	AA446869	ESTs	7.3
RC_N21321_i	N21321	ESTs	7.3
RC_AA121315	AA121315	ESTs	7.2
RC_R65593_s	R65593	Homo sapiens mRNA for kynurenine 3-monooxygenase	7.2
RC_AA427950	AA427950	EST - RC_AA427950	7.2
RC_AA088458	AA088458	ESTs Weakly similar to !!!! ALU SUBFAMILY J	7.2
RC_AA432130	AA432130	ESTs Moderately similar to !!!! ALU SUBFAMILY SX	7.2
RC_AA234921	AA234921	ESTs	7.2
AA310967_s	AA310967	ESTs Weakly similar to T04A8.11 [C.elegans]	7.1
RC_AA236177	AA236177	ESTs	7.1
RC_AA282143	AA282143	H.sapiens mRNA for melanoma growth regulatory protein	7.1
RC_AA283003	AA283003	ESTs	7.1
RC_AA421158	AA421158	ESTs	7.1
RC_T10082_f	T10082	ESTs	7.1
C00225_s	C00225	ESTs Highly similar to HYPOTHETICAL 52.8 KD	7.1
RC_AA258482	AA258482	Human mRNA for zinc finger protein complete cds	7.1
RC_AA287870	AA287870	Lymphotoxin-beta	7.1
RC_AA410373	AA410373	ESTs	7.1
RC_F13694_f	F13694	ESTs	7.1
RC_N29431	N29431	EST - RC_N29431	7.1
RC_N67239	N67239	ESTs	7.1
RC_AA449351	AA449351	ESTs Weakly similar to similar to deoxyribose-phosphate	7.0
RC_Z40345	Z40345	ESTs Weakly similar to T06D8.5 [C.elegans]	7.0

FIGURE 4 (CONT.)

RC_N34686	N34686	Homo sapiens clone 23915 mRNA sequence	7.0
RC_AA310499	AA310499	ESTs	7.0
RC_D57389_f	D57389	EST	7.0
RC_N71704	N71704	ESTs	6.9
RC_AA410441	AA410441	ESTs	6.9
RC_AA505093	AA505093	ESTs	6.9
U48705_ma1	U48705	Receptor protein-tyrosine kinase EDDR1	6.9
RC_AA419461	AA419461	ESTs	6.8
RC_AA411204	AA411204	ESTs	6.8
RC_AA496569	AA496569	ESTs Highly similar to VALYL-TRNA SYNTHETASE	6.8
RC_AA346385	AA346385	ESTs Highly similar to putative hydrophobic domain in	6.8
RC_D51229_f	D51229	Human clone 23589 mRNA sequence	6.8
RC_AA127818	AA127818	ESTs	6.8
RC_H18428_s	H18428	ESTs Weakly similar to !!!! ALU SUBFAMILY J	6.8
RC_F02254_s	F02254	H.sapiens mRNA for FAST kinase	6.8
RC_AA416876	AA416876	ESTs Weakly similar to TRANSFORMATION-	6.8
RC_AA446966	AA446966	EST	6.8
RC_N50550	N50550	Homo sapiens mRNA for Efs1 complete cds	6.7
L27841	L27841	Human autoantigen pericentriol material 1 (PCM-1)	6.7
U30246	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter	6.7
RC_AA034069	AA034069	ESTs	6.7
RC_T92935	T92935	ESTs	6.7
U24169	U24169	Human JTV-1 (JTV-1) mRNA complete cds	6.7
RC_H99935_s	H99935	Interleukin 6 signal transducer (gp130 oncostatin M	6.7
RC_AA435849	AA435849	ESTs Moderately similar to unknown protein [H.sapiens]	6.7
RC_AA127058	AA127058	ESTs	6.7
M11718	M11718	Collagen type V alpha	6.7
RC_AA283198	AA283198	ESTs	6.6
RC_R51988	R51988	ESTs	6.6
RC_AA505141	AA505141	ESTs	6.6
RC_D60341	D60341	ESTs	6.6
RC_N26904	N26904	ESTs Highly similar to FK506-BINDING PROTEIN	6.6
RC_R40606	R40606	ESTs Highly similar to SKD3 [M.musculus]	6.6
RC_T03790	T03790	ESTs	6.6
RC_W72455	W72455	ESTs	6.6
RC_AA098834	AA098834	Nuclear factor of kappa light polypeptide gene enhancer in	6.6
RC_AA421782	AA421782	ESTs	6.6
AA236384	AA236384	ESTs Highly similar to COP1 REGULATORY PROTEIN	6.5
RC_AA431085	AA431085	EST	6.5
W49521	W49521	Human prolyl 4-hydroxylase alpha (II) subunit mRNA	6.5

FIGURE 4 (CONT.)

RC_AA446591	AA446591	ESTs	6.5
RC_R06700	R06700	ESTs	6.5
RC_AA100364	AA100364	ESTs	6.5
X54326	X54326	MULTIFUNCTIONAL AMINOACYL-TRNA	6.4
U89606	U89606	Human pyridoxal kinase mRNA complete cds	6.4
RC_AA195651	AA195651	EST	6.4
RC_T15991	T15991	ESTs	6.4
RC_AA430211	AA430211	ESTs	6.4
RC_T17119	T17119	ESTs	6.4
RC_AA157814	AA157814	ESTs	6.3
X70649	X70649	Homo sapiens DDX1 gene complete CDS	6.3
RC_H57330	H57330	EST	6.3
D81608	D81608	H.sapiens mRNA for RNA polymerase II subunit	6.3
RC_R65826	R65826	Homo sapiens mRNA for KIAA0549 protein partial cds	6.3
RC_AA621169	AA621169	ESTs	6.3
L77701	L77701	Homo sapiens COX17 mRNA complete cds	6.3
RC_AA443658	AA443658	Homo sapiens lamin B receptor homolog TM7SF2	6.3
W19662	W19662	ESTs	6.3
RC_D20168	D20168	Human mRNA for KIAA0050 gene complete cds	6.3
RC_N48166	N48166	ESTs	6.3
RC_AA024664	AA024664	Human NADH:ubiquinone oxidoreductase subunit B13	6.2
RC_AA279943	AA279943	ESTs	6.2
RC_AA098874	AA098874	ESTs	6.2
X86018	X86018	H.sapiens mRNA for MUF1 protein	6.2
RC_AA412106	AA412106	ESTs	6.2
RC_AA621721	AA621721	ESTs	6.2
U40271	U40271	Protein-tyrosine kinase 7	6.2
X52150_ma1_s	X52150	Arylsulfatase A	6.2
RC_AA152178	AA152178	ESTs	6.2
RC_N38959_f	N38959	Homo sapiens chaperonin containing t-complex	6.2
L37747_s	L37747	LAMIN B1	6.1
U78525	U78525	Human eukaryotic translation initiation factor (eIF3)	6.1
RC_T77733_s	T77733	Tubulin gamma polypeptide	6.1
RC_D20280	D20280	ESTs	6.1
RC_W69807	W69807	ESTs Highly similar to GOLIATH PROTEIN [Drosophila	6.1
RC_AA405505	AA405505	Homo sapiens mRNA for putative RNA helicase 3' end	6.1
RC_AA133199	AA133199	ESTs	6.1
RC_H55748	H55748	ESTs	6.1
RC_AA479933	AA479933	ESTs	6.1
RC_AA448349	AA448349		

FIGURE 4 (CONT.)

RC_AA600257	AA600257	ERGIC-53 PROTEIN PRECURSOR	6.1
RC_R99978	R99978	ESTs Weakly similar to line-1 protein ORF2 [H.sapiens]	6.1
AA455331	AA455331	ESTs	6.1
RC_H55915	H55915	ESTs Weakly similar to LINE-1 REVERSE	6.1
RC_AA398740	AA398740	ESTs	6.1
RC_AA521080	AA521080	ESTs	6.1
RC_AA416568	AA416568	ESTs	6.1
RC_N92593	N92593	ESTs	6.1
L32137	L32137	Human germline oligomeric matrix protein (COMP)	6.1
RC_AA609277	AA609277	ESTs	6.0
RC_R33663_s	R33663	ESTs	6.0
RC_AA521103	AA521103	ESTs	6.0
RC_AA406137	AA406137	EST	6.0
U73514	U73514	Homo sapiens short chain L-3-hydroxyacyl-CoA	6.0
RC_T16660	T16660	ESTs	6.0
J04177	J04177	Collagen type XI alpha 1	6.0
RC_W38407	W38407	ESTs	5.9
RC_N26391	N26391	ESTs	5.9
RC_AA292655	AA292655	ESTs	5.9
RC_Z41619_s	Z41619	ESTs Weakly similar to keratin 8 type II cytoskeletal	5.9
RC_AA223730	AA223730	ESTs	5.9
RC_T88953	T88953	ESTs	5.9
RC_N50744	N50744	ESTs	5.9
RC_W63563_s	W63563	Homo sapiens scaffold attachment factor B (SAF-B)	5.9
HG3748-	TIGR - HG3748-	EST - HG3748-HT4018	5.9
RC_AA430673	AA430673	ESTs	5.8
RC_AA463740	AA463740	ESTs	5.8
M25753	M25753	Cyclin B1	5.8
RC_AA279292	AA279292	ESTs	5.8
RC_AA427925	AA427925	ESTs Weakly similar to PROCOLLAGEN ALPHA 1(II)	5.8
RC_AA287665	AA287665	ESTs	5.8
RC_AA422007	AA422007	ESTs	5.8
RC_AA425379	AA425379	ESTs	5.8
RC_T67463_s	T67463	CATHEPSIN K PRECURSOR	5.8
RC_AA441801	AA441801	ESTs	5.8
RC_H89987_s	H89987	Human multidrug resistance-associated protein homolog	5.8
RC_H94843	H94843	ESTs	5.8
RC_N80183	N80183	ESTs	5.8
U65932	U65932	Human extracellular matrix protein 1 (ECM1) mRNA	5.8
RC_N27563	N27563	ESTs	5.7

FIGURE 4 (CONT.)

RC_F09058	F09058	ESTs	5.7
RC_R02572	R02572	Fibronectin 1	5.7
RC_AA442763	AA442763	ESTs Highly similar to G2/MITOTIC-SPECIFIC	5.7
RC_AA149624	AA149624	Homo sapiens mRNA for follistain-related protein (FRP)	5.7
RC_AA459945	AA459945	Homo sapiens mRNA for KIAA0585 protein partial cds	5.7
RC_R09166	R09166	ESTs	5.7
	M34677	FACTOR VIII INTRON 22 PROTEIN	5.7
RC_AA478794	AA478794	ESTs	5.7
	W30943	ESTs	5.7
RC_AA192334	AA192334	ESTs	5.7
RC_AA454562	AA454562	Homo sapiens clone 24522 mRNA sequence	5.7
	U56402	ESTs	5.7
	AA443251	EST	5.7
RC_AA207105	AA207105	ESTs	5.7
RC_AA609473	AA609473	ESTs	5.7
RC_H54430	H54430	EST	5.7
RC_R85829	R85829	EST - HG2981-HT3125	5.7
	HG2981-TIGR - HG2981-	ESTs	5.6
RC_AA232956	AA232956	EST - U91327	5.6
	U91327	ESTs	5.6
RC_N51590_s	N51590	Homo sapiens KIAA0431 mRNA partial cds	5.6
RC_AA406169	AA406169	ESTs	5.6
RC_AA147884	AA147884	ESTs	5.6
RC_AA453987	AA453987	ESTs	5.6
RC_AA040154	AA040154	ESTs Moderately similar to TYKi protein [M.musculus]	5.6
RC_T23528	T23528	Human mRNA for KIAA0124 gene partial cds	5.6
	D50914	H.sapiens DAP-1 mRNA	5.6
	X76105	EST	5.6
RC_AA149754	AA149754	ESTs	5.6
RC_AA397919	AA397919	ESTs	5.6
RC_AA398212	AA398212	Guanine nucleotide binding protein (G protein) beta	5.6
RC_AA416986	AA416986	EST	5.6
RC_AA435936	AA435936	ESTs	5.6
RC_T95057_f	T95057	ESTs Weakly similar to T12D8.i [C.elegans]	5.6
	AA116095	ESTs	5.6
	AA477214	Homo sapiens clone 23736 mRNA sequence	5.6
RC_AA398264	AA398264	Human fatty acid amide hydrolase mRNA complete cds	5.6
RC_AA435742	AA435742	ESTs	5.6
RC_AA452842	AA452842	Integral transmembrane protein 1	5.6
RC_AA482269	AA482269		

FIGURE 4 (CONT.)

RC_AA436819	AA436819	ESTs	5.6
RC_N93797	N93797	ESTs	5.6
RC_AA443602	AA443602	ESTs	5.5
RC_AA609996	AA609996	ESTs Highly similar to Surf-4 protein [M.musculus]	5.5
RC_AA075200	AA075200	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-	5.5
RC_AA195517	AA195517	ESTs Weakly similar to !!!! ALU SUBFAMILY J	5.5
X02874	X02874	(2'-5') oligoadenylate synthetase E	5.5
RC_AA085589	AA085589	ESTs Highly similar to TRANSLATION INITIATION	5.5
RC_H99500	H99500	Homo sapiens mRNA for follistain-related protein (FRP)	5.5
RC_R43883	R43883	ESTs	5.5
M24486	M24486	Procollagen-proline 2-oxoglutarate 4-dioxygenase (proline	5.5
RC_AA115535	AA115535	ESTs	5.5
RC_AA280840	AA280840	ESTs	5.5
RC_N22015	N22015	ESTs	5.5
RC_AA021182	AA021182	EST	5.5
RC_N21032	N21032	Human fibroblast activation protein mRNA complete cds	5.5
U09278	U09278	ESTs	5.4
RC_AA251973	AA251973	Laminin receptor (2H5 epitope)	5.4
RC_H75933_i	H75933	EST	5.4
RC_T81310	T81310	SIGNAL TRANSDUCER AND ACTIVATOR OF	5.4
M97936	M97936	ESTs	5.4
RC_AA242757	AA242757	ESTs	5.4
RC_W92001	W92001	EST - RC_AA398721	5.4
RC_AA398721	AA398721	ESTs	5.4
RC_AA448410	AA448410	H.sapiens mRNA for SYT	5.4
RC_AA479348	AA479348	ESTs Weakly similar to weak similarity to ribosomal	5.4
C02170	C02170	ESTs	5.4
RC_AA437225	AA437225	ESTs	5.4
RC_N51917	N51917	Homo sapiens clone 23870 mRNA sequence	5.4
RC_AA293773	AA293773	ESTs	5.4
RC_AA449357	AA449357	ESTs	5.4
RC_R41294_s	R41294	CD44 antigen (cell adhesion molecule)	5.4
RC_W45275_f	W45275	ESTs Weakly similar to 50S RIBOSOMAL PROTEIN L20	5.3
RC_AA447213	AA447213	ESTs	5.3
RC_AA135809	AA135809	ESTs	5.3
RC_AA191524	AA191524	ESTs	5.3
RC_AA399477	AA399477	ESTs	5.3
RC_H80749	H80749	Human germline oligomeric matrix protein (COMP)	5.3
RC_N94385_s	N94385	EST - RC_AA157811	5.3
RC_AA157811	AA157811		

FIGURE 4 (CONT.)

RC_AA425154	AA425154	ESTs	5.3
RC_AA284565	AA284565	ESTs	5.3
RC_AA287022	AA287022	Thymidine kinase 1 soluble	5.3
RC_AA464860	AA464860	Homo sapiens Jak2 kinase mRNA complete cds	5.3
RC_AA401428	AA401428	NUCLEAR PORE COMPLEX PROTEIN NUP214	5.3
RC_AA394071	AA394071	Homo sapiens gamma2-adaptin (G2AD) mRNA complete	5.3
RC_AA195036	AA195036	Human Ro/SSA ribonucleoprotein homolog (RoRet)	5.3
RC_AA465191	AA465191	ESTs	5.3
RC_AA476293	AA476293	ESTs Weakly similar to DNA-DIRECTED RNA	5.3
U59877	U59877	Human low-Mr GTP-binding protein (RAB31) mRNA	5.3
X03363	X03363	ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE	5.3
RC_AA621714	AA621714	ESTs	5.2
RC_AA026682	AA026682	Topoisomerase (DNA) II alpha (170kD)	5.2
RC_AA025370	AA025370	ESTs	5.2
RC_AA005262	AA005262	Homo sapiens DNA sequence from PAC 262D12 on	5.2
RC_AA403116	AA403116	Homo sapiens U-snRNP-associated cyclophilin (USA-	5.2
RC_AA488280	AA488280	EST - RC_AA488280	5.2
RC_H96392	H96392	ESTs	5.2
RC_N73861	N73861	EST - RC_N73861	5.2
X17644	X17644	G1 to S phase transition 1	5.2
H87319	H87319	Protein kinase C substrate 80K-H	5.2
RC_AA452857	AA452857	ESTs	5.2
RC_R92205	R92205	ESTs	5.2
RC_N54321	N54321	EST	5.2
RC_AA279160	AA279160	ESTs	5.2
RC_AA599140	AA599140	ESTs Moderately similar to ZINC FINGER PROTEIN 7	5.2
RC_AA609891	AA609891	EST	5.2
RC_R05312_s	R05312	ESTs	5.2
RC_R59183_f	R59183	ESTs	5.2
RC_W45302	W45302	ESTs Highly similar to HYPOTHETICAL HELICASE	5.2
RC_W59961_s	W59961	Human mRNA for KIAA0389 gene complete cds	5.1
RC_AA481453	AA481453	ESTs	5.1
RC_R42036	R42036	ESTs	5.1
RC_AA434152	AA434152	ESTs	5.1
RC_W60180	W60180	ESTs	5.1
RC_N79612	N79612	ESTs	5.1
RC_AA487449	AA487449	EST - RC_AA487449	5.1
RC_R43543	R43543	ESTs	5.1
RC_AA284518	AA284518	ESTs	5.1
RC_N98461	N98461	ESTs	5.1

FIGURE 4 (CONT.)

Y09912_mal	Y09912	H.sapiens mRNA for AP-2 beta transcription factor	5.1
RC_AA491465	AA491465	ESTs	5.1
RC_AA436673	AA436673	ESTs	5.1
RC_N73808_f	N73808	ESTs	5.0
J05614	J05614	EST - J05614	5.0
RC_F10496_f	F10496	H.sapiens 40 kDa protein kinase related to rat ERK2	5.0
J00314	J00314	Homo sapiens clone 24703 beta-tubulin mRNA complete	5.0
RC_AA085676	AA085676	ESTs Weakly similar to TYL [H.sapiens]	5.0
RC_AA236356	AA236356	ESTs	5.0
RC_AA252395	AA252395	ESTs	5.0
RC_N33927_s	N33927	"Homo sapiens mRNA for histone H2B clone pJG4-5-	5.0
RC_AA262179	AA262179	ESTs	5.0
RC_AA211400	AA211400	ESTs	5.0
M80244	M80244	INTEGRAL MEMBRANE PROTEIN E16	5.0
M16336	M16336	CD2 antigen (T cell surface antigen T11)	5.0
AA479995	AA479995	Homo sapiens mRNA for KIAA0583 protein partial cds	5.0
D82419	D82419	ESTs Highly similar to UBIQUITIN-CONJUGATING	5.0
RC_AA055892	AA055892	ESTs	5.0
RC_AA281451	AA281451	ESTs	5.0
U62392	U62392	Homo sapiens zinc finger protein mRNA complete cds	5.0
RC_AA172056	AA172056	ESTs	5.0
RC_AA287095	AA287095	EST - RC_AA287095	5.0
RC_AA425691	AA425691	ESTs	5.0
RC_AA426376	AA426376	ESTs	5.0
RC_AA446000	AA446000	ESTs	5.0
RC_AA478951	AA478951	EST	5.0
RC_F02080_f	F02080	ESTs	5.0
RC_T79815	T79815	ESTs Weakly similar to !!!! ALU SUBFAMILY J	5.0
RC_F10945	F10945	Polypyrimidine tract binding protein (hnRNP I)	4.9
C01169	C01169	Homo sapiens clone 23915 mRNA sequence	4.9
RC_AA490830	AA490830	ESTs	4.9
RC_AA133756	AA133756	ESTs	4.9
RC_H24044	H24044	Protein phosphatase 2 (formerly 2A) catalytic subunit	4.9
RC_R41772	R41772	EST	4.9
RC_T59338	T59338	EST - RC_T59338	4.9
D21255	D21255	Cadherin 11 (OB-cadherin)	4.9
RC_AA234559	AA234559	ESTs	4.9
RC_N34893	N34893	ESTs Highly similar to HYPOTHETICAL 47.8 KD	4.9
RC_AA191512	AA191512	ESTs	4.8
RC_W60007_s	W60007	Human mRNA for KIAA0203 gene complete cds	4.8

FIGURE 4 (CONT.)

RC_AA400513	AA400513	ESTs	4.8
RC_N94362	N94362	EST	4.8
RC_AA406081	AA406081	ESTs	4.8
RC_AA448158	AA448158	EST	4.8
RC_AA404352	AA404352	ESTs	4.7
AA075599	AA075599	ESTs Highly similar to NADH-UBIQUINONE	4.7
RC_AA026356	AA026356	ESTs	4.7
RC_AA157836	AA157836	ESTs	4.7
RC_AA196549	AA196549	ESTs	4.7
RC_AA417321	AA417321	ESTs Weakly similar to CALMODULIN [D.melanogaster]	4.7
RC_AA418074	AA418074	ESTs	4.7
RC_N32919	N32919	ESTs	4.7
RC_AA620795	AA620795	ESTs	4.6
U18321	U18321	H.sapiens DAP-3 mRNA	4.6
RC_H97012	H97012	ESTs Weakly similar to L8004.7 gene product	4.6
RC_AA177051	AA177051	EST - RC_AA177051	4.6
RC_AA453483	AA453483	ESTs	4.6
X17059	X17059	ARYLAMINE N-ACETYLTRANSFERASE	4.6
M34458_ma1	M34458	LAMIN B1	4.6
RC_N68921	N68921	ESTs	4.6
RC_AA464853	AA464853	ESTs Weakly similar to T01G9.4 [C.elegans]	4.5
RC_AA210722	AA210722	EST	4.5
RC_AA461507	AA461507	ESTs	4.5
RC_T40841	T40841	ESTs	4.5
RC_N71076	N71076	EST	4.5
X57766	X57766	Human stromelysin-3 mRNA	4.5
RC_AA255605	AA255605	Homo sapiens spindle pole body protein spc97 homolog	4.5
RC_AA443634	AA443634	Homo sapiens ubiquitin conjugating enzyme G2	4.5
RC_T97307	T97307	EST - RC_T97307	4.4
X02419_ma1	X02419	Urokinase-type plasminogen activator	4.4
RC_AA430124	AA430124	ESTs	4.4
RC_AA405569	AA405569	Human fibroblast activation protein mRNA complete cds	4.4
RC_AA227900	AA227900	H.sapiens mRNA homologous to S. cerevisiae RAD54	4.4
AA422025_s	AA422025	ESTs	4.4
RC_AA346495	AA346495	ESTs Moderately similar to !!!! ALU SUBFAMILY J	4.4
RC_AA386260	AA386260	EST	4.4
RC_AA398155	AA398155	ESTs	4.4
RC_AA453466	AA453466	ESTs	4.4
RC_AA463726	AA463726	Homo sapiens mRNA for JM27 protein complete CDS	4.4
RC_C20981	C20981	ESTs Highly similar to CHOLINE DEHYDROGENASE	4.4

FIGURE 4 (CONT.)

	R70801	EST	4.4
RC_R70801_s	U28386	RAG (recombination activating gene) cohort 1	4.4
U28386	AA206497	PROTEASOME COMPONENT C9	4.4
RC_AA206497	U21090	Human DNA polymerase delta small subunit mRNA	4.3
U21090	AA453176	Human protein kinase ATR mRNA complete cds	4.3
RC_AA453176	AA235112	ESTs	4.3
RC_AA235112	U73379	Human cyclin-selective ubiquitin carrier protein mRNA	4.3
U73379	U24389	Human lysyl oxidase-like protein mRNA complete cds	4.3
U24389	D42073	Human mRNA for reticulocalbin complete cds	4.3
D42073	H18947	ESTs	4.2
RC_H18947	H90161	ESTs	4.2
RC_H90161_s	H25577	ESTs Highly similar to CYTOCHROME P450 IVB1	4.2
RC_H25577	S74445	Cellular retinoic acid-binding protein [human skin mRNA	4.2
S74445	AA419200	ESTs	4.2
RC_AA419200	AA227959	Human cysteine protease Mch2 isoform alpha (Mch2)	4.2
RC_AA227959	AA416931	ESTs	4.2
RC_AA416931	U74612	Human putative M phase phosphoprotein 2 (MPP2) mRNA	4.2
U74612	R46482	ESTs	4.2
RC_R46482	X62534	High-mobility group (nonhistone chromosomal) protein 2	4.2
X62534	M15796	Proliferating cell nuclear antigen	4.2
M15796	D54296	Human mRNA for KIAA0255 gene complete cds	4.1
RC_D54296_f	AA398369	ESTs	4.1
RC_AA398369	AA464707	ESTs	4.1
RC_AA464707	AA478799	H.sapiens mRNA for BS69 protein	4.1
RC_AA478799	AA496369	ESTs	4.1
RC_AA496369	U50648	Protein kinase interferon-inducible double stranded RNA	4.1
U50648	N66818	ESTs	4.1
RC_N66818	AA448347	Annexin XI (56kD autoantigen)	4.1
RC_AA448347	AA193297	ESTs	4.0
AA193297	AA287596	ESTs	4.0
RC_AA287596	AA228026	ESTs Highly similar to PBDX protein [H.sapiens]	4.0
RC_AA228026	AA421041	ESTs	4.0
RC_AA421041	W87752	Small inducible cytokine A5 (RANTES)	4.0
RC_W87752_s	X94563	EST - X94563_xpt2_r	4.0
X94563_xpt2_r	U29463	Cytochrome B561	4.0
U29463	AA287325	ESTs	4.0
RC_AA287325	R44709	Homo sapiens mRNA for RB18A protein	3.9
RC_R44709	AA256837	ESTs	3.9
RC_AA256837	W45572	ADP-ribosylation factor 1	3.9
RC_W45572_f	AA482224	ESTs Weakly similar to No definition line found	3.9
RC_AA482224			

FIGURE 4 (CONT.)

RC_AA416627	AA416627	ESTs	3.9
RC_AA485360	AA485360	EST	3.9
RC_AA459960	AA459960	ESTs Weakly similar to D9481.16 gene product	3.8
RC_AA224324	AA224324	ESTs	3.8
RC_AA132366	AA132366	Homo sapiens mRNA for SPOP	3.8
RC_AA599244	AA599244	Homo sapiens mRNA for KIAA0530 protein partial cds	3.8
RC_AA465094	AA465094	ESTs Weakly similar to nemo form II [D.melanogaster]	3.8
RC_N41018	N41018	Human mRNA for prepro cortistatin like peptide complete	3.8
W46488	W46488	Homo sapiens Amplified in Breast Cancer (AIB1) mRNA	3.8
RC_N98525	N98525	Homo sapiens tumorous imaginal discs protein Tid56	3.8
RC_N74501	N74501	ESTs	3.8
RC_AA425652	AA425652	ESTs	3.8
RC_AA485451	AA485451	EST	3.8
RC_AA133527	AA133527	ESTs Moderately similar to The KIAA0138 gene product	3.8
RC_AA287642	AA287642	Human mRNA for KIAA0078 gene complete cds	3.8
RC_AA232183	AA232183	ESTs Weakly similar to !!!! ALU SUBFAMILY J	3.7
RC_N67102_s	N67102	ESTs	3.7
M25077	M25077	Human 60-kdal ribonucleoprotein (Ro) mRNA complete	3.7
RC_AA424486	AA424486	ESTs	3.7
RC_W45728	W45728	ESTs Highly similar to HETEROGENEOUS NUCLEAR	3.7
RC_AA399547	AA399547	ESTs	3.7
RC_AA598661	AA598661	ESTs	3.7
Y12394	Y12394	Homo sapiens importin-alpha homolog (SRP1gamma)	3.7
M14219	M14219	Decorin	3.7
RC_H04339	H04339	ESTs	3.7
RC_AA435840	AA435840	Homo sapiens mRNA for high mobility group protein	3.6
RC_F02450	F02450	ESTs Moderately similar to unknown protein [H.sapiens]	3.6
RC_N91887_s	N91887	Homo sapiens mRNA for NB thymosin beta complete cds	3.6
RC_AA401758	AA401758	ESTs Weakly similar to !!!! ALU SUBFAMILY SQ	3.6
RC_W73788	W73788	ESTs	3.6
RC_N63823	N63823	ESTs	3.6
RC_N67603	N67603	ESTs Weakly similar to hypothetical L1 protein	3.6
RC_AA461492	AA461492	ESTs	3.6
RC_AA521240	AA521240	ESTs	3.6
RC_N93967	N93967	EST	3.6
D82558	D82558	Homo sapiens KB07 protein mRNA partial cds	3.5
RC_N36835	N36835	ESTs	3.5
RC_AA159181	AA159181	ESTs Weakly similar to Lpa8p [S.cerevisiae]	3.5
RC_AA126951	AA126951	ESTs Weakly similar to DNA-directed RNA polymerase	3.5
RC_AA398450	AA398450	H.sapiens mRNA for synaptonemal complex lateral	3.5

FIGURE 4 (CONT.)

RC_AA112063	AA112063	ESTs Weakly similar to PRE-MRNA SPLICING	3.5
RC_R70167	R70167	ESTs	3.5
RC_AA034365	AA034365	NUCLEAR PORE GLYCOPROTEIN P62	3.5
RC_X75346	X75346	H.sapiens mRNA for MAP kinase activated protein kinase	3.5
RC_AA083069	AA083069	EST - RC_AA083069	3.5
RC_AA404593	AA404593	ESTs	3.5
RC_AA412739	AA412739	EST	3.5
RC_AA447626	AA447626	EST	3.5
RC_AA453787	AA453787	Human TFIIB related factor hBRF (HBRF) mRNA	3.5
RC_AA599106	AA599106	EST - RC_AA599106	3.5
RC_H72283_s	H72283	Human mRNA for KIAA0265 gene partial cds	3.5
RC_N90859	N90859	ESTs	3.5
RC_L38961	L38961	Integral transmembrane protein 1	3.5
X69141	X69141	FARNESYL-DIPHOSPHATE	3.5
RC_R63734	R63734	ESTs	3.5
RC_AA164209	AA164209	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-	3.4
RC_AA449417	AA449417	Homo sapiens mRNA for putative glucosyltransferase	3.4
RC_H88639	H88639	ESTs	3.4
RC_AA411448	AA411448	ESTs	3.4
RC_AA258203	AA258203	ESTs	3.4
RC_AA100470	AA100470	ESTs	3.4
RC_N29740	N29740	ESTs	3.4
RC_N34895	N34895	Phosphoribosyl pyrophosphate amidotransferase	3.4
RC_AA442070	AA442070	Homo sapiens mRNA for putative methyltransferase	3.4
AA115397	AA115397	EST	3.4
RC_F10326_f	F10326	H.sapiens mRNA for diubiquitin	3.4
RC_N33920	N33920	ESTs	3.4
RC_AA429917	AA429917	EST	3.4
RC_AA453164	AA453164	Human hSIAI12 mRNA complete cds	3.4
RC_AA029042	AA029042	EST - L47276	3.4
L47276	L47276	DNA topoisomerase 1	3.4
U07806	U07806	L-UBC	3.4
S81003	S81003	ESTs Weakly similar to LINE-1 REVERSE	3.3
RC_AA232535	AA232535	ESTs	3.3
RC_AA490899	AA490899	Homo sapiens cDNA similar to RNA binding protein C.	3.3
RC_R45356	R45356	ESTs	3.3
RC_AA047896	AA047896	Homo sapiens sodium/myo-inositol cotransporter	3.3
RC_F09353	F09353	ESTs	3.3
RC_N67437	N67437	ESTs	3.3
RC_AA116036	AA116036		

FIGURE 4 (CONT.)

RC_AA453159	AA453159	Human kinesin-like spindle protein HKSP (HKSP) mRNA	3.3
RC_AA496051	AA496051	ESTs	3.3
RC_W85861	W85861	ESTs Weakly similar to ZK1058.4 [C.elegans]	3.3
RC_R24237_f	R24237	ESTs	3.3
AD000092_cds	AD000092	Homo sapiens DNA from chromosome 19p13.2 cosmids	3.3
RC_W44735	W44735	ESTs	3.3
RC_AA435847	AA435847	EST - RC_AA435847	3.3
RC_N34059	N34059	EST - RC_N34059	3.3
RC_N58172	N58172	ESTs Weakly similar to !!!! ALU SUBFAMILY SC	3.3
AA421213	AA421213	ESTs Weakly similar to F28F8.3 [C.elegans]	3.2
RC_N35385	N35385	ESTs	3.2
RC_T15665	T15665	ESTs Weakly similar to HYPOTHETICAL 139.1 KD	3.2
RC_W46255	W46255	ESTs	3.2
RC_AA490969	AA490969	ESTs	3.2
RC_F09315	F09315	Homo sapiens mRNA for KIAA0583 protein partial cds	3.2
RC_AA169379	AA169379	ESTs	3.2
RC_AA211941	AA211941	Homo sapiens polyadenylate binding protein-interacting	3.2
M86852	M86852	Peroxisomal membrane protein 3 (35kD Zellweger	3.2
RC_AA134965	AA134965	ESTs	3.2
RC_R60192_s	R60192	Peroxisomal biogenesis factor 7	3.2
D84145	D84145	Human WS-3 mRNA complete cds	3.2
Z97054_xpt2	Z97054	Human mRNA for KIAA0312 gene partial cds	3.2
RC_AA232939	AA232939	ESTs	3.2
RC_T65797	T65797	ESTs Weakly similar to Pin1 protein [H.sapiens]	3.2
RC_W33134_s	W33134	ESTs	3.2
RC_AA609423	AA609423	ESTs	3.2
L07515	L07515	HETEROCHROMATIN PROTEIN 1 HOMOLOG	3.2
RC_R67996	R67996	ESTs	3.2
RC_AA422079	AA422079	ESTs Weakly similar to RAR-RESPONSIVE PROTEIN	3.2
U51586	U51586	Human siah binding protein 1 (SiahBP1) mRNA partial cds	3.2
U37547	U37547	Human IAP homolog B (MIHB) mRNA complete cds	3.2
U81554	U81554	Homo sapiens signal recognition particle 72 (SRP72)	3.2
T40327_s	T40327	ESTs	3.2
RC_N78572	N78572	EST - RC_N78572	3.2
RC_AA448213	AA448213	Human myogenic repressor I-mf (MDFI) mRNA complete	3.2
RC_AA047036	AA047036	ESTs	3.1
RC_W72967	W72967	ESTs	3.1
RC_N69331	N69331	Peptidylprolyl isomerase C (cyclophilin C)	3.1
RC_W44928	W44928	ESTs	3.1
RC_AA150043	AA150043	ESTs	3.1

FIGURE 4 (CONT.)

	D60208	ESTs	3.1
RC_D60208_f	AA401687	Homo sapiens ribonuclease P protein subunit p20 (RPP20)	3.1
RC_AA401687	N21626	ESTs	3.1
RC_N21626	S66431	Homo sapiens clone 23592 mRNA sequence	3.1
S66431	X17620	NUCLEOSIDE DIPHOSPHATE KINASE A	3.1
X17620	X59798	Cyclin D1 (PRAD1 parathyroid adenomatosis 1)	3.1
X59798	AA232874	EST	3.1
RC_AA232874	AA291259	ESTs	3.1
RC_AA291259	D87466	Human mRNA for KIAA0276 gene partial cds	3.1
D87466	AA398360	EST	3.1
RC_AA398360	X70944	PTB-ASSOCIATED SPLICING FACTOR	3.0
X70944_s	AA099719	ESTs	3.0
RC_AA099719	S50223	HKR-T1	3.0
S50223	AA251738	H.sapiens mRNA for TAFII100 protein	3.0
RC_AA251738	Y12065	Homo sapiens mRNA for nucleolar protein hNop56	3.0
Y12065	AA406577	ESTs	3.0
RC_AA406577	N47204	ESTs Weakly similar to C50F4.12 [C.elegans]	3.0
RC_N47204	W80482	ESTs	3.0
RC_W80482	AA423827	ESTs	3.0
RC_AA423827	AA227932	ESTs	3.0
RC_AA227932	W46286	ESTs Weakly similar to ZK1058.5 [C.elegans]	3.0
RC_W46286_s	AA386264	ESTs Highly similar to ribosome-binding protein p34	3.0
RC_AA386264	X74801	H.sapiens Cctg mRNA for chaperonin	3.0
X74801	AA152305	Interferon (gamma)-induced cell line protein 10 from	3.0
RC_AA152305	R36548	ESTs	3.0
RC_R36548	N32333	Homo sapiens M962 protein spliced isoform 2 mRNA	2.9
RC_N32333	N36881	ESTs	2.9
RC_N36881	H16790	ESTs	2.9
RC_H16790	AA393164	Homo sapiens mammaglobin B precursor mRNA complete	2.9
AA393164_s	AA399164	ESTs	2.9
RC_AA399164	AA164293	ESTs	2.9
RC_AA164293	D60061	ESTs	2.9
RC_D60061_s	AA203523	ESTs Weakly similar to coded for by C. elegans cDNA	2.9
RC_AA203523	AA195936	ESTs Weakly similar to W02D9.2 [C.elegans]	2.9
RC_AA195936	T25732	Human mRNA for KIAA0252 gene partial cds	2.9
RC_T25732_f	AA426120	EST - RC_AA426120	2.9
RC_AA426120	AA485214	DNA-BINDING PROTEIN NEFA PRECURSOR	2.9
RC_AA485214	U40714	Human tyrosyl-tRNA synthetase mRNA complete cds	2.9
U40714	AA213506	ESTs	2.9
RC_AA213506	R50840	H.sapiens mRNA for ras-related GTP-binding protein	2.9
RC_R50840			

FIGURE 4 (CONT.)

RC_R97040	R97040	ESTs	2.9
M28211	M28211	Homo sapiens GTP-binding protein (RAB4) mRNA	2.9
AA452011	AA452011	ESTs Highly similar to deduced protein product shows	2.9
RC_AA228020	AA228020	Homo sapiens splicing factor (CC1.3) mRNA complete cds	2.9
T54762_s	T54762	ESTs	2.9
RC_AA242834	AA242834	ESTs	2.9
RC_F13779	F13779	ESTs	2.9
RC_AA206088	AA206088	ESTs	2.9
RC_AA292747	AA292747	ESTs	2.9
RC_AA400725	AA400725	ESTs	2.9
RC_H97677_s	H97677	EST - HG110-HT110	2.9
HG110-HT110	TIGR - HG110-	Thymidylate synthase	2.9
D00596	D00596	ESTs Weakly similar to T08A11.2 [C.elegans]	2.9
RC_AA279420	AA279420	ESTs	2.9
RC_AA399264	AA399264	ESTs Moderately similar to rabkinesin-6 [M.musculus]	2.9
RC_AA179845	AA179845	ESTs Weakly similar to ORF YOR285w [S.cerevisiae]	2.8
RC_AA411532	AA411532	H.sapiens mRNA for M-phase phosphoprotein mpp5	2.8
RC_AA292765	AA292765	HEAT SHOCK 70 KD PROTEIN 1	2.8
RC_AA609501	AA609501	ESTs	2.8
RC_AA478596	AA478596	ESTs	2.8
RC_N48715	N48715	EST	2.8
RC_AA412497	AA412497	ESTs Weakly similar to !!!! ALU SUBFAMILY J	2.8
RC_AA480103	AA480103	Homo sapiens eps8 binding protein e3B1 mRNA complete	2.8
AF006516	AF006516	ESTs	2.8
RC_AA128407	AA128407	ESTs Weakly similar to Similar to S.cerevisiae	2.8
RC_AA425606	AA425606	ESTs	2.8
RC_AA232231	AA232231	EST - RC_T63857	2.8
RC_T63857	T63857	ESTs	2.8
RC_AA488432	AA488432	Natural resistance-associated macrophage protein 2	2.8
RC_R49327	R49327	ESTs	2.8
RC_AA405512	AA405512	ESTs	2.8
RC_R79617	R79617	Human mRNA for clathrin-like protein complete cds	2.8
RC_AA310729	AA310729	EST - RC_AA446572	2.8
RC_AA446572	AA446572	ESTs	2.8
RC_AA486407	AA486407	ESTs Weakly similar to elastin like protein	2.8
RC_R39234_r	R39234	Uracil-DNA glycosylase	2.8
RC_AA425900	AA425900	PUTATIVE 60S RIBOSOMAL PROTEIN	2.8
RC_F03605_f	F03605	Human neutral amino acid transporter B mRNA complete	2.8
U53347	U53347	Human splicing factor SRp30c mRNA complete cds	2.8
U30825	U30825		

FIGURE 4 (CONT.)

RC_N21159	N21159	Homo sapiens forkhead protein (FKHRL1) mRNA	2.8
RC_H24460_s	H24460	FK506-binding protein 4 (59kD)	2.8
RC_D80710_f	D80710	ESTs Weakly similar to transmembrane protein [H.sapiens]	2.8
X76732	X76732	DNA-BINDING PROTEIN NEFA PRECURSOR	2.8
RC_AA001409	AA001409	ESTs	2.8
RC_N92915	N92915	ESTs	2.8
RC_N29325	N29325	ESTs Highly similar to 47 KD PROTEIN [Pseudomonas	2.8
RC_AA609200	AA609200	EST - RC_AA609200	2.8
RC_R41933	R41933	ESTs	2.8
RC_AA262768	AA262768	ESTs	2.8
RC_R46025	R46025	ESTs	2.8
RC_AA164687	AA164687	ESTs	2.7
RC_AA424031	AA424031	ESTs	2.7
RC_N23663	N23663	ESTs	2.7
RC_W69160	W69160	ESTs	2.7
RC_N25798	N25798	ESTs	2.7
RC_AA431333	AA431333	ESTs Highly similar to Ras inhibitor [H.sapiens]	2.7
RC_R54112	R54112	ESTs	2.7
RC_F02863	F02863	ESTs Moderately similar to !!!! ALU SUBFAMILY SQ	2.7
RC_W80750	W80750	ESTs	2.7
RC_AA461509	AA461509	ESTs Weakly similar to putative p150 [H.sapiens]	2.7
RC_AA620586	AA620586	ESTs	2.7
L11669	L11669	Human tetracycline transporter-like protein mRNA	2.7
RC_AA291269	AA291269	ESTs	2.7
RC_W87747	W87747	ESTs	2.7
K02777	K02777	T cell receptor alpha-chain	2.7
X89986	X89986	H.sapiens mRNA for NBK apoptotic inducer protein	2.7
RC_AA125969	AA125969	ESTs Weakly similar to F35G12.9 [C.elegans]	2.7
RC_AA449718	AA449718	ESTs Weakly similar to ZINC FINGER PROTEIN 42	2.7
RC_R02354	R02354	ESTs	2.7
RC_AA425725	AA425725	ESTs Weakly similar to serine protein kinase SRPK1	2.7
RC_R71481	R71481	ESTs	2.7
D63391	D63391	Human mRNA for platelet activating factor	2.7
RC_AA126743	AA126743	ESTs	2.7
U33052	U33052	Human lipid-activated protein kinase PRK2 mRNA	2.7
M96982	M96982	SPLICING FACTOR U2AF 35 KD SUBUNIT	2.7
X16396	X16396	NAD-DEPENDENT	2.7
L12350	L12350	Thrombospondin 2	2.7
AA215333	AA215333	ESTs	2.7
RC_AA102520	AA102520	ESTs Highly similar to HYPOTHETICAL 31.6 KD	2.7

FIGURE 4 (CONT.)

RC_N68869	N68869	ESTs	2.6
RC_W85712	W85712	ESTs Weakly similar to PROCOLLAGEN ALPHA 2(IV)	2.6
RC_AA176121	AA176121	ESTs	2.6
RC_AA001402	AA001402	Homo sapiens 15 kDa selenoprotein mRNA complete cds	2.6
RC_N51316	N51316	ESTs Highly similar to elastin like protein	2.6
L03411	L03411	Radin blood group	2.6
D79997	D79997	Human mRNA for KIAA0175 gene complete cds	2.6
L04490	L04490	Homo sapiens (clone CC6) NADH-ubiquinone	2.6
RC_AA412112	AA412112	EST - RC_AA412112	2.6
RC_AA417956	AA417956	ESTs	2.6
RC_AA453624	AA453624	Human terminal transferase mRNA complete cds	2.6
RC_N63210	N63210	ESTs	2.6
RC_N92948_s	N92948	Human IEF SSP 9502 mRNA complete cds	2.6
RC_AA447553	AA447553	ESTs	2.6
AF001294	AF001294	Homo sapiens IPL (IPL) mRNA complete cds	2.6
Z49099	Z49099	H.sapiens mRNA for spermine synthase	2.6
RC_AA598648	AA598648	Human mRNA for transcriptional activator hSNF2b	2.6
RC_AA447617	AA447617	ESTs	2.6
RC_AA293300	AA293300	ESTs Weakly similar to semaphorin C [M.musculus]	2.6
RC_R50333_i	R50333	ESTs	2.6
AB000115	AB000115	Homo sapiens mRNA expressed in osteoblast complete cds	2.6
D63881	D63881	Human mRNA for KIAA0160 gene partial cds	2.6
T39176_s	T39176	ESTs Weakly similar to ZK1058.4 [C.elegans]	2.6
RC_N46252	N46252	ESTs	2.6
RC_N33516	N33516	Homo sapiens nibrin (NBS) mRNA complete cds	2.6
RC_N48790	N48790	ESTs Moderately similar to !!!! ALU SUBFAMILY SX	2.6
RC_H98655	H98655	Homo sapiens nibrin (NBS) mRNA complete cds	2.6
RC_AA242758	AA242758	Human breast cancer estrogen regulated LIV-1 protein	2.6
RC_AA130349	AA130349	ESTs	2.5
RC_AA262491	AA262491	ESTs	2.5
RC_N70646	N70646	ESTs	2.5
RC_AA490882	AA490882	ESTs	2.5
RC_AA610073	AA610073	ESTs	2.5
RC_N67187_s	N67187	ESTs	2.5
RC_AA404957	AA404957	Matrix Gla protein	2.5
RC_T70541	T70541	ESTs	2.5
RC_AA236489	AA236489	ESTs	2.5
RC_AA284372	AA284372	ESTs	2.5
RC_D60374_f	D60374	EST - RC_D60374_f	2.5
RC_AA069547	AA069547	EST - RC_AA069547	2.5

FIGURE 4 (CONT.)

RC_AA398280	AA398280	ESTs	2.5
RC_N93000	N93000	ESTs	2.5
RC_AA291503	AA291503	EST	2.5
RC_AA446100	AA446100	ESTs	2.5
RC_W47183	W47183	ESTs	2.5
L00205	L00205	KERATIN TYPE II CYTOSKELETAL 6D	2.5
RC_AA369027	AA369027	ESTs	2.5
RC_N66158	N66158	ESTs	2.5
RC_AA428179	AA428179	EST	2.5
X70218	X70218	Protein phosphatase 4 (formerly X) catalytic subunit	2.5
AB002308	AB002308	Human mRNA for KIAA0310 gene complete cds	2.5
RC_AA416877	AA416877	ESTs	2.5
RC_AA262730	AA262730	ESTs	2.5
X54941	X54941	CDC28 protein kinase 1	2.5
D43948	D43948	Human mRNA for KIAA0097 gene complete cds	2.5
M23379	M23379	GTPase-activating protein ras p21 (RASA)	2.5
X85373	X85373	H.sapiens mRNA for Sm protein G	2.5
U16306	U16306	LARGE FIBROBLAST PROTEOGLYCAN	2.5
T39763_s	T39763	ESTs	2.5
RC_H12634	H12634	ESTs	2.5
RC_AA251587	AA251587	Homo sapiens mRNA for KIAA0530 protein partial cds	2.5
RC_AA160890	AA160890	Human mRNA for KIAA0389 gene complete cds	2.5
RC_N21677	N21677	ESTs	2.5
RC_AA191424	AA191424	ESTs	2.5
RC_AA451707	AA451707	ESTs	2.5
RC_AA045083	AA045083	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE	2.5
RC_AA252672	AA252672	Homo sapiens diphthamide biosynthesis protein-2 (DPH2)	2.4
W79060	W79060	ESTs Highly similar to ribosome-binding protein p34	2.4
RC_AA262651	AA262651	ESTs	2.4
RC_AA399047	AA399047	ESTs	2.4
RC_AA456646	AA456646	ESTs	2.4
RC_AA258601	AA258601	EST - RC_AA258601	2.4
RC_N51260_s	N51260	Human mRNA for KIAA0240 gene partial cds	2.4
X13482	X13482	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'	2.4
AA504223	AA504223	ESTs Highly similar to CHROMOSOME	2.4
RC_R37778	R37778	ESTs	2.4
RC_W31919	W31919	EST	2.4
RC_AA487207	AA487207	EST - RC_AA487207	2.4
RC_AA599674	AA599674	ESTs Weakly similar to F08G12.1 [C.elegans]	2.4
RC_Z40898	Z40898	ESTs	2.4

FIGURE 4 (CONT.)

RC_AA286942	AA286942	EST - RC_AA286942	2.4
RC_AA371604	AA371604	Human Rho-associated coiled-coil containing protein	2.4
RC_AA223209	AA223209	ESTs Weakly similar to D9481.16 gene product	2.4
RC_AA218663	AA218663	ESTs Weakly similar to U1 SMALL NUCLEAR	2.4
RC_AA449458	AA449458	ESTs	2.4
D38555	D38555	Human mRNA for KIAA0079 gene complete cds	2.4
U73477	U73477	HLA-DR ASSOCIATED PROTEIN I	2.4
X60382_ma1	X60382	COL10A1	2.4
X84373	X84373	NUCLEAR FACTOR RIP140	2.4
M55542	M55542	Guanylate binding protein 1 interferon-inducible 67kD	2.4
S82597_ma1	S82597	H.sapiens mRNA for UDP-GalNAc:polypeptide N-	2.4
M90516	M90516	Glutamine-fructose-6-phosphate transaminase	2.4
D87684	D87684	Human mRNA for KIAA0242 gene partial cds	2.4
D82348	D82348	Human mRNA for 5-aminoimidazole-4-carboxamide-1-	2.4
RC_AA190993	AA190993	ESTs	2.4
RC_N69352	N69352	Homo sapiens mRNA for ATP-dependent RNA helicase	2.4
AA434329	AA434329	ESTs	2.4
RC_T29681_f	T29681	Human serine kinase mRNA complete cds	2.4
RC_AA279799	AA279799	ESTs	2.4
RC_T25896	T25896	ESTs	2.4
RC_AA147708	AA147708	ESTs Highly similar to VACUOLAR ATP SYNTHASE	2.4
RC_AA039887	AA039887	ESTs	2.4
RC_AA455239	AA455239	ESTs Highly similar to CHROMOSOME	2.4
RC_Z39909	Z39909	ESTs Moderately similar to ZINC FINGER PROTEIN	2.3
AA330771_s	AA330771	Human protein-tyrosine phosphatase (HU-PP-1) mRNA	2.3
RC_AA173223	AA173223	ESTs	2.3
R81830	R81830	Homo sapiens breast cancer putative transcription factor	2.3
RC_AA031814	AA031814	ESTs Weakly similar to R01H10.8 [C.elegans]	2.3
RC_AA010065	AA010065	CDC28 protein kinase 2	2.3
RC_W23625_s	W23625	ESTs Highly similar to HYPOTHETICAL TRP-ASP	2.3
RC_F02907	F02907	ESTs	2.3
RC_N94581	N94581	ESTs	2.3
RC_AA069285	AA069285	ESTs Weakly similar to PROBABLE UBIQUITIN	2.3
RC_AA450116	AA450116	ESTs	2.3
RC_N33063	N33063	ESTs Highly similar to GAG POLYPROTEIN [Avian	2.3
RC_T87807_s	T87807	ESTs	2.3
RC_W49574	W49574	ESTs Moderately similar to !!!! ALU SUBFAMILY SQ	2.3
RC_AA250737	AA250737	ESTs	2.3
RC_AA425749	AA425749	ESTs	2.3
U77180	U77180	Human mRNA for EBI1-ligand chemokine complete cds	2.3

FIGURE 4 (CONT.)

RC_AA024658	AA024658	ESTs	2.3
RC_AA037657	D00591	Chromosome condensation 1	2.3
RC_AA037410	X94453	Pyrroline-5-carboxylate synthetase (glutamate gamma-	2.3
RC_AA459673	AA459673	ESTs Highly similar to CIIROMOSOME	2.3
RC_AA428647	AA428647	ESTs	2.3
RC_R52088	R52088	EST - RC_R52088	2.3
RC_X54199	X54199	Phosphoribosylglycinamide formyltransferase	2.3
RC_N49284_s	N49284	MYB PROTO-ONCOGENE PROTEIN	2.3
U37022_ma1	U37022	Human cyclin-dependent protein kinase mRNA complete	2.3
D26156	D26156	Human mRNA for transcriptional activator hSNF2b	2.3
U72514	U72514	Human C2f mRNA complete cds	2.3
S79873	S79873	Lysosomal-associated membrane protein 2	2.3
U47077	U47077	Human DNA-dependent protein kinase catalytic subunit	2.3
U59423	U59423	Human chromosome 4 Mad homolog Smad1 mRNA	2.3
J05633	J05633	Integrin beta-5 subunit	2.3
Z48042	Z48042	H.sapiens mRNA encoding GPI-anchored protein p137	2.3
RC_AA037657	AA037657	ESTs	2.3
RC_N29888	N29888	Human NAD+-specific isocitrate dehydrogenase beta	2.3
RC_AA251776	AA251776	ESTs	2.3
RC_AA282568	AA282568	ESTs Weakly similar to F25H2.6 [C.elegans]	2.3
RC_AA236951	AA236951	ESTs	2.3
RC_AA464423	AA464423	ESTs Weakly similar to !!!! ALU SUBFAMILY J	2.3
RC_AA037410	AA037410	Human DNA sequence from PAC 127B20 on chromosome	2.3
RC_R63652	R63652	ESTs	2.3
RC_N66857	N66857	ESTs	2.2
RC_AA280588	AA280588	ESTs	2.2
RC_AA436477	AA436477	ESTs	2.2
RC_AA028028	AA028028	ESTs	2.2
RC_N39148	N39148	ESTs	2.2
RC_AA485223	AA485223	ESTs	2.2
RC_AA011556	AA011556	ESTs	2.2
RC_AA053636	AA053636	ESTs	2.2
RC_AA148516	AA148516	ESTs	2.2
RC_AA495924	AA495924	ESTs	2.2
RC_AA131692	AA131692	ESTs	2.2
RC_N90401	N90401	ESTs	2.2
RC_AA436613	AA436613	Homo sapiens mRNA transcriptional unit N143	2.2
RC_AA397921	AA397921	ESTs Moderately similar to metastasis-associated gene	2.2
RC_AA251766	AA251766	ESTs	2.2
RC_F09328	F09328		

FIGURE 4 (CONT.)

RC_T15674_f	T15674	ESTs	2.2
RC_AA416735	AA416735	ESTs	2.2
RC_AA423827	AA423827	ESTs	2.2
RC_AA600200	AA600200	ESTs	2.2
RC_H84658_s	H84658	ESTs	2.2
RC_H99261_s	H99261	Human DNA from overlapping chromosome 19 cosmids	2.2
RC_T10060	T10060	ESTs	2.2
AA043160	AA043160	ESTs	2.2
RC_AA059214	AA059214	ESTs Moderately similar to neurexophilin 2 [M.musculus]	2.2
RC_AA490237	AA490237	EST - RC_AA490237	2.2
RC_AA227856	AA227856	H.sapiens mRNA for HOXC9 protein exon 1	2.2
RC_H28428	H28428	ESTs	2.2
RC_AA076328	AA076328	Cyclin-dependent kinase inhibitor 2A (melanoma p16	2.2
RC_F13690_s	F13690	ESTs Weakly similar to ZNF127-Xp [H.sapiens]	2.2
RC_AA287320	AA287320	ESTs	2.2
RC_AA287833	AA287833	ESTs	2.2
RC_AA430726	AA430726	EST - RC_AA430726	2.2
RC_N93618	N93618	ESTs	2.2
RC_T59686_s	T59686	ESTs	2.2
U09770	U09770	Human cysteine-rich heart protein (hCRHP) mRNA	2.2
RC_R72008	R72008	ESTs Weakly similar to Diff33 gene product [H.sapiens]	2.2
RC_N94606	N94606	ESTs	2.2
RC_D80237_s	D80237	Homo sapiens Arp2/3 protein complex subunit p20-Arc	2.2
U09510	U09510	Glycyl-tRNA synthetase	2.2
U86782	U86782	Human 26S proteasome-associated pad1 homolog (POH1)	2.2
X70476	X70476	COATOMER BETA' SUBUNIT	2.2
RC_AA417030	AA417030	Homo sapiens protein regulating cytokinesis 1 (PRC1)	2.2
RC_AA446949	AA446949	ESTs	2.2
RC_AA236516	AA236516	ESTs Weakly similar to ISOLEUCYL-TRNA	2.2
R78119	R78119	ESTs	2.2
RC_AA150088	AA150088	Homo sapiens vesicle transport related protein mRNA	2.2
RC_AA043353	AA043353	ESTs Highly similar to UBIQUITIN-CONJUGATING	2.2
RC_AA126719	AA126719	ESTs	2.2
RC_AA403121	AA403121	ESTs	2.1
RC_N64378	N64378	ESTs	2.1
RC_AA158132	AA158132	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces	2.1
RC_AA253031	AA253031	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-	2.1
RC_Z99394_s	Z99394	ESTs Moderately similar to !!!! ALU SUBFAMILY SP	2.1
RC_AA400820	AA400820	ESTs	2.1
RC_W20391_s	W20391	Human mRNA for kinesin-related protein partial cds	2.1

FIGURE 4 (CONT.)

RC_AA281780	AA281780	ESTs Weakly similar to HYPOTHETICAL 46.4 KD	2.1
RC_R91380_s	R91380	H. sapiens RNA for CLCN3	2.1
U51205	U51205	Human COP9 homolog (HCOP9) mRNA complete cds	2.1
U58090	U58090	Human Hs-cul-4A mRNA partial cds	2.1
X70944	X70944	PTB-ASSOCIATED SPLICING FACTOR	2.1
U60808	U60808	Human CDP-diacylglycerol synthase (CDS) mRNA	2.1
AA460077	AA460077	ESTs	2.1
RC_AA251909	AA251909	Homo sapiens MAD3-like protein kinase mRNA complete	2.1
RC_AA134063	AA134063	ESTs	2.1
RC_H38246_s	H38246	ESTs Weakly similar to similar to S. cerevisiae LAG1	2.1
RC_AA451712	AA451712	ESTs	2.1
RC_H80737_s	H80737	ESTs	2.1
M74099	M74099	Cut (Drosophila)-like 1 (CCAAT displacement protein)	2.1
RC_AA018587	AA018587	ESTs Weakly similar to !!!! ALU SUBFAMILY SP	2.1
RC_AA291137	AA291137	ESTs	2.1
RC_AA426060	AA426060	ESTs	2.1
RC_AA427662	AA427662	ESTs	2.1
RC_AA465148	AA465148	ESTs	2.1
RC_AA610039	AA610039	ESTs	2.1
RC_N72113	N72113	ESTs	2.1
RC_W32470	W32470	ESTs	2.1
RC_AA620464	AA620464	Human mRNA for KIAA0331 gene complete cds	2.1
RC_AA609869	AA609869	ESTs	2.1
U61232	U61232	Human tubulin-folding cofactor E mRNA complete cds	2.1
M30938	M30938	ATP-DEPENDENT DNA HELICASE II 86 KD	2.1
D13988	D13988	Homo sapiens mRNA for GDP dissociation inhibitor beta	2.1
U67122	U67122	Human ubiquitin-homology domain protein PIC1 mRNA	2.1
X70683	X70683	SRY (sex determining region Y)-box 4	2.1
RC_N22222	N22222	ESTs	2.1
RC_AA393695	AA393695	LARGE FIBROBLAST PROTEOGLYCAN	2.1
RC_W37384_i	W37384	Homo sapiens testis-specific nm23 homolog mRNA	2.1
RC_F01986_f	F01986	EST	2.1
RC_N95837	N95837	Homo sapiens clone 24651 mRNA sequence	2.1
RC_N24968	N24968	Homo sapiens vacuolar H(+)-ATPase subunit mRNA	2.1
RC_AA598452	AA598452	ESTs	2.0
RC_AA287388	AA287388	ESTs	2.0
RC_AA487202	AA487202	ESTs	2.0
RC_F02651	F02651	ESTs	2.0
AF015913	AF015913	Homo sapiens SKB1Hs mRNA complete cds	2.0
RC_AA476582	AA476582	ESTs Highly similar to SIGNAL RECOGNITION	2.0

FIGURE 4 (CONT.)

RC_R68425	R68425	ESTs	2.0
RC_W80467	W80467	ESTs	2.0
RC_D53392_f	D53392	ESTs Weakly similar to PEREGRIN [H.sapiens]	2.0
RC_Z39053	Z39053	ESTs	2.0
RC_N91246	N91246	ESTs	2.0
Z29090	Z29090	PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC	2.0
AA443460	AA443460	ESTs	2.0
RC_AA045481	AA045481	ESTs	2.0
W28362	W28362	ESTs	2.0
RC_AA233177	AA233177	ESTs	2.0
RC_T90746	T90746	ESTs	2.0
RC_H78241_s	H78241	H.sapiens mRNA for novel member of serine-arginine	2.0
RC_AA443596	AA443596	ESTs	2.0
RC_AA453255	AA453255	ESTs	2.0
X69636	X69636	Human mRNA for KIAA0393 gene complete cds	2.0
RC_AA047265	AA047265	Homo sapiens mRNA for osteoblast specific cysteine-rich	2.0
RC_AA188981	AA188981	Homo sapiens retinoblastoma-associated protein HEC	2.0
RC_H11938	H11938	EST - RC_H11938	2.0
RC_T23539	T23539	ESTs Highly similar to zinc finger protein [M.musculus]	2.0
RC_AA405838	AA405838	ESTs	2.0
RC_AA426375	AA426375	ESTs Highly similar to PRE-MRNA SPLICING FACTOR	2.0
RC_N24954	N24954	ESTs	2.0
D78586	D78586	CAD PROTEIN	2.0
U34044	U34044	Human selenium donor protein (selD) mRNA complete cds	2.0
RC_AA621122	AA621122	ESTs	2.0
RC_Z40810	Z40810	ESTs	2.0
RC_AA127716	AA127716	Homo sapiens unknown mRNA complete cds	2.0
RC_AA237022	AA237022	ESTs	2.0
RC_AA479139	AA479139	Acid phosphatase 1 soluble	2.0
U05340	U05340	Human p55CDC mRNA complete cds	2.0
RC_AA417909	AA417909	ESTs	2.0
RC_AA181657	AA181657	ESTs	2.0
L37347	L37347	Natural resistance-associated macrophage protein 2	2.0
X92896	X92896	H.sapiens mRNA for ITBA2 protein	2.0
M23263	M23263	Androgen receptor (dihydrotestosterone receptor testicular	2.0
U37519	U37519	Aldehyde dehydrogenase 8	2.0
D28364	D28364	EST - D28364	2.0
D86978	D86978	Human mRNA for KIAA0225 gene partial cds	2.0
Z24724	Z24724	H.sapiens polyA site DNA	2.0
U39840	U39840	Human hepatocyte nuclear factor-3 alpha (HNF-3 alpha)	2.0

FIGURE 4 (CONT.)

RC_AA136884	AA136884	ESTs	2.0
	T63174	ESTs	2.0
T63174_s		ESTs	2.0
RC_N50963	N50963	Human mRNA for KIAA0178 gene partial cds	2.0
	D80000	Homo sapiens meltrin-L precursor (ADAM12) mRNA	2.0
D80000		ESTs	2.0
RC_R73567	R73567	ESTs	2.0
RC_N70520	N70520	ESTs	2.0
RC_N22162	N22162	ESTs	2.0
RC_AA476312	AA476312	ESTs	2.0
RC_AA521474	AA521474	Core-binding factor beta subunit	2.0
	L20298	H.sapiens mRNA for RNA polymerase II subunit	2.0
	Z47727	Human mRNA for clathrin coat assembly protein-like	2.0
	U91932	ESTs	1.9
RC_AA173417	AA173417	ESTs	1.9
RC_AA287834	AA287834	ESTs Highly similar to FK506-BINDING PROTEIN	1.9
	W80763	ESTs	1.9
RC_AA112679	AA112679	ESTs	1.9
RC_AA233261	AA233261	H.sapiens mRNA for transcriptional intermediary factor 2	1.9
RC_T77464	T77464	ESTs Weakly similar_to No definition line found	1.9
RC_AA227463	AA227463	Homo sapiens thyroid hormone receptor-associated protein	1.9
	D50920	Human mRNA for KIAA0020 gene complete cds	1.9
	D13645	ESTs Highly similar to HYPOTHETICAL 16.5 KD	1.9
RC_AA233168	AA233168	ESTs	1.9
RC_AA227963	AA227963	ESTs	1.9
RC_AA451898	AA451898	ESTs	1.9
RC_AA302745	AA302745	ESTs	1.9
RC_N23393	N23393	EST - RC_W37933	1.9
RC_W37933	W37933	ESTs Weakly similar to Sp140 protein [H.sapiens]	1.9
RC_AA504832	AA504832	EST	1.9
RC_AA446918	AA446918	ESTs	1.9
RC_N47469	N47469	ESTs Weakly similar to siah binding protein 1 [H.sapiens]	1.9
RC_T89703	T89703	H.sapiens mRNA for 2.19 gene	1.9
X55448_cds1	X55448	ESTs Highly similar to UBIQUITIN-CONJUGATING	1.9
RC_AA257972	AA257972	ESTs Weakly similar to T13F2.1 [C.elegans]	1.9
RC_Z40715	Z40715	ESTs Weakly similar to Y53C12A.3 [C.elegans]	1.9
	AA464013	ESTs Highly similar to HYPOTHETICAL 37.2 KD	1.9
RC_W95063	W95063	Signal recognition particle 19 kD protein	1.9
	X12791	Homo sapiens ICT1 (alias DS-1) mRNA	1.9
	X81788	Murine leukemia viral (bmi-1) oncogene homolog	1.9
	L13689	Human protein kinase mRNA complete cds	1.9
	L33801		

FIGURE 4 (CONT.)

U76638	U76638	Human BRCA1-associated RING domain protein	1.9
HG174-HT174	TIGR - HG174-	EST - HG174-HT174	1.9
X58072	X58072	GATA-binding protein 3	1.9
U05237	U05237	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA	1.9
M21259	M21259	Small nuclear ribonucleoprotein polypeptide E	1.9
RC_AA149585	AA149585	ESTs	1.9
AA115058_s	AA115058	ESTs	1.9
RC_AA236453	AA236453	EST	1.9
RC_T25867	T25867	Human heterochromatin protein HP1Hs-gamma mRNA	1.9
U26312	U26312	Human Gu protein mRNA partial cds	1.9
U41387	U41387	ESTs	1.9
RC_AA496000	AA496000	ESTs	1.9
RC_AA489046	AA489046	ESTs	1.9
RC_AA278653	AA278653	CATHEPSIN K PRECURSOR	1.9
X82153	X82153	ESTs	1.9
RC_AA403008	AA403008	PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1	1.9
D12485	D12485	ESTs	1.9
H44386_s	H44386	ESTs	1.9
RC_N46423	N46423	ESTs	1.9
RC_N55336	N55336	ESTs	1.9
RC_AA497052	AA497052	ESTs Moderately similar to !!!! ALU SUBFAMILY SQ	1.8
RC_N26855	N26855	ESTs	1.8
RC_N52006	N52006	Homo sapiens mRNA for p115 complete cds	1.8
RC_Z40332	Z40332	ESTs	1.8
RC_AA028074	AA028074	ESTs Weakly similar to F25D7.1 [C.elegans]	1.8
RC_AA279171	AA279171	Homo sapiens clone 23770 mRNA sequence	1.8
RC_AA251982	AA251982	ESTs	1.8
AA455001_s	AA455001	ESTs Moderately similar to ALR [H.sapiens]	1.8
RC_AA599219	AA599219	Human mRNA for KIAA0208 gene complete cds	1.8
RC_W84790_s	W84790	ESTs	1.8
RC_H94248	H94248	ESTs	1.8
RC_AA234765	AA234765	ESTs Weakly similar to PROBABLE E5 PROTEIN	1.8
RC_N35583	N35583	ESTs Moderately similar to 60S RIBOSOMAL PROTEIN	1.8
AA099241	AA099241	ESTs	1.8
RC_AA436192	AA436192	ESTs	1.8
RC_AA420988	AA420988	ESTs Highly similar to DOSAGE COMPENSATION	1.8
RC_F02990	F02990	Centromere protein A (17kD)	1.8
U14518	U14518	ESTs	1.8
RC_AA232103	AA232103	ESTs	1.8
RC_AA398319	AA398319		

FIGURE 4 (CONT.)

RC_W52225	W52225	ESTs	1.8
RC_AA063460	AA063460	Gastrin-releasing peptide	1.8
RC_AA447603	AA447603	EST	1.8
RC_AA401274	AA401274	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-	1.8
RC_F04989	F04989	ESTs	1.8
RC_T96595	T96595	EST - RC_T96595	1.8
AF000430	AF000430	Homo sapiens mRNA for Dnm1p/Vps1p-like protein	1.8
L76937_mal	L76937	Homo sapiens Werner syndrome gene complete cds	1.8
U72263	U72263	Exostoses (multiple) 2	1.8
L25876	L25876	Human protein phosphatase (KAP1) mRNA complete cds	1.8
W68502	W68502	ESTs	1.8
RC_AA005108	AA005108	ESTs	1.8
RC_W72876	W72876	ESTs	1.8
RC_AA457566	AA457566	ESTs	1.8
X75962	X75962	OX40L RECEPTOR PRECURSOR	1.8
RC_AA232104	AA232104	ESTs Highly similar to transcription factor ARF6 chain B	1.8
RC_AA417962	AA417962	ESTs Highly similar to GERANYLGERANYL	1.8
RC_D59894	D59894	ESTs	1.8
RC_AA598988	AA598988	ESTs Moderately similar to HYPOTHETICAL 52.2 KD	1.8
RC_W88983	W88983	Human RNA-binding protein CUG-BP/hNab50 (NAB50)	1.8
M36429	M36429	Human transducin beta-2 subunit mRNA complete cds	1.8
X92098	X92098	H.sapiens mRNA for transmembrane protein rmp24	1.8
U70322	U70322	Human transportin (TRN) mRNA complete cds	1.8
M63180	M63180	Threonyl-tRNA synthetase	1.8
U32986	U32986	Damage-specific DNA binding protein 1 (127 kD)	1.8
U65928	U65928	V-jun avian sarcoma virus 17 oncogene homolog	1.8
L10910	L10910	Homo sapiens splicing factor (CC1.3) mRNA complete cds	1.8
RC_R41281	R41281	Homo sapiens DNJ3/CPR3 mRNA complete cds	1.8
RC_N50050	N50050	ESTs	1.8
RC_AA460350	AA460350	ESTs	1.8
RC_AA292066	AA292066	ESTs Weakly similar to C01H6.7 [C.elegans]	1.8
RC_AA291923	AA291923	ESTs	1.8
RC_AA411144	AA411144	ESTs	1.8
RC_AA436171	AA436171	ESTs	1.8
RC_AA251758	AA251758	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3)	1.8
RC_AA406478	AA406478	ESTs	1.8
RC_AA191353	AA191353	ESTs	1.8
D13630	D13630	Human mRNA for KIAA0005 gene complete cds	1.8
X65488	X65488	HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN	1.8
RC_AA131584	AA131584	ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces	1.8

FIGURE 4 (CONT.)

RC_AA283743	AA283743	ESTs Moderately similar to YY1-associated factor 2	1.8
RC_AA056588	AA056588	ESTs	1.7
RC_AA180321	AA180321	ESTs Weakly similar to W04D2.6 [C.elegans]	1.7
RC_AA262957	AA262957	ESTs	1.7
RC_AA234767	AA234767	ESTs	1.7
RC_AA479961	AA479961	ESTs	1.7
RC_T03865	T03865	ESTs	1.7
RC_N51226	N51226	Collagen type IV alpha 3	1.7
RC_AA056249	AA056249	ESTs	1.7
RC_H17620	H17620	ESTs	1.7
RC_H73608_s	H73608	ESTs	1.7
RC_H23230	H23230	ESTs	1.7
RC_AA171529	AA171529	ESTs	1.7
RC_AA470140	AA470140	ESTs	1.7
RC_AA459005	AA459005	ESTs	1.7
RC_AA425439	AA425439	EST	1.7
RC_AA609364	AA609364	ESTs	1.7
RC_N31598	N31598	ESTs	1.7
RC_T57317	T57317	Human Chromosome 16 BAC clone CIT987SK-A-735G6	1.7
W55890	W55890	ESTs	1.7
RC_N50831	N50831	ESTs	1.7
RC_AA280687	AA280687	EST	1.7
RC_AA111879	AA111879	ESTs	1.7
RC_AA116075	AA116075	Human GABA-A receptor pi subunit mRNA complete cds	1.7
U95367	U95367	Homo sapiens exportin t mRNA complete cds	1.7
RC_AA598447	AA598447	EST - RC_W38150	1.7
RC_W38150	W38150	Homo sapiens clone 23797 and 23917 mRNA partial cds	1.7
RC_AA232315	AA232315	ESTs	1.7
RC_R39923	R39923	ESTs	1.7
RC_AA410972	AA410972	Homo sapiens vesicle trafficking protein sec22b mRNA	1.7
W23469	W23469	ESTs Highly similar to C10 [H.sapiens]	1.7
RC_AA287091	AA287091	ESTs	1.7
RC_AA291260	AA291260	Human arginine-rich nuclear protein mRNA complete cds	1.7
RC_AA465690	AA465690	ESTs	1.7
RC_AA453465	AA453465	H.sapiens mRNA for 55.11 binding protein	1.7
D78151	D78151	TRANSLATIONAL INITIATION FACTOR 2 GAMMA	1.7
L19161	L19161	Human histone 2A-like protein (H2A/l) mRNA complete	1.7
U90551	U90551	Homo sapiens protein phosphatase 2A B56-epsilon (PP2A)	1.7
L76703	L76703	EST - HG4557-HT4962	1.7
HG4557-	TIGR - HG4557-		

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FIGURE 4 (CONT.)

		Cathepsin B	1.7
RC_N58561_s	N58561	ESTs	1.7
RC_H15436	H15436	Chaperonin containing T-complex subunit 6	1.7
L27706	L27706	ESTs	1.7
RC_W85888	W85888	ESTs	1.7
RC_AA479362	AA479362	ESTs	1.7
D31161_s	D31161	ESTs	1.7
RC_AA035143	AA035143	Homo sapiens putative fatty acid desaturase MLD mRNA	1.7
AF002668	AF002668	ESTs	1.7
RC_AA416733	AA416733	Proto-oncogene AML1 {alternative products}	1.7
RC_N92860_s	N92860	ESTs	1.7
RC_R93068	R93068	ESTs	1.7
RC_W19222	W19222	EST - RC_AA599267	1.7
RC_AA599267	AA599267	ESTs	1.7
RC_AA410894	AA410894	ESTs	1.7
RC_AA609053	AA609053	EST	1.7
RC_AA400080	AA400080	ESTs	1.7
RC_AA286891	AA286891	ESTs Moderately similar to HYPOTHETICAL 66.5 KD	1.7
RC_N31952	N31952	ESTs	1.7
RC_AA421773	AA421773	Homo sapiens clone 1400 unknown protein mRNA partial	1.7
RC_N90029	N90029	ESTs	1.7
RC_AA156142	AA156142	Homo sapiens drp1 mRNA complete cds	1.7
RC_AA132514	AA132514	ESTs	1.6
RC_AA465222	AA465222	ESTs Weakly similar to Similar to S.cerevisiae	1.6
AA426176	AA426176	ESTs	1.6
RC_AA155803	AA155803	Homo sapiens thyroid receptor interactor (TRIP3) mRNA	1.6
RC_T64937_s	T64937	ESTs Highly similar to GONADOTROPIN-RELEASING	1.6
RC_AA243052	AA243052	ESTs Weakly similar to CLEAVAGE STIMULATION	1.6
RC_AA456437	AA456437	Homo sapiens mRNA for KIAA0286 gene partial cds	1.6
RC_AA424524	AA424524	EST	1.6
RC_AA252360	AA252360	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4	1.6
W58247_s	W58247	ESTs	1.6
RC_AA599622	AA599622	H.sapiens mRNA for unknown protein expressed in	1.6
X89059	X89059	ESTs	1.6
RC_W04698	W04698	ESTs Weakly similar to L8004.7 gene product	1.6
RC_N73865	N73865	Homo sapiens cyclin T2a mRNA complete cds	1.6
RC_T23820	T23820	Homo sapiens mRNA for GDP dissociation inhibitor beta	1.6
RC_AA099589	AA099589	Human enhancer of zeste homolog 2 (EZH2) mRNA	1.6
U61145	U61145	EST	1.6
RC_AA151708	AA151708	ESTs	1.6
H19378	H19378		

FIGURE 4 (CONT.)

RC_AA417970	AA417970	ESTs	1.6
RC_R10720	R10720	EST	1.6
AA256106	AA256106	ESTs	1.6
U12424_s	U12424	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	1.6
RC_W73820	W73820	ESTs	1.6
RC_AA167708	AA167708	ESTs	1.6
AA187579	AA187579	ESTs Weakly similar to Yel007c-ap [S.cerevisiae]	1.6
RC_R15743	R15743	ESTs	1.6
RC_N69014_s	N69014	Homo sapiens SOX22 protein (SOX22) mRNA complete	1.6
RC_Z38919	Z38919	ESTs	1.6
AB002343	AB002343	Human mRNA for KIAA0345 gene complete cds	1.6
RC_AA521186	AA521186	ESTs	1.6
RC_AA258205	AA258205	Homo sapiens DNA polymerase zeta catalytic subunit	1.6
D14811	D14811	Human mRNA for KIAA0110 gene complete cds	1.6
U59286	U59286	Homo sapiens interferon stimulated T-cell alpha	1.6
M34079	M34079	PROBABLE 26S PROTEASE SUBUNIT TBP-1	1.6
RC_AA026418	AA026418	ESTs	1.6
RC_N26259	N26259	ESTs Weakly similar to NADH-UBIQUINONE	1.6
D50840	D50840	Human mRNA for ceramide glucosyltransferase complete	1.6
M97856	M97856	Nuclear autoantigenic sperm protein (histone-binding)	1.6
U10323	U10323	Human nuclear factor NF45 mRNA complete cds	1.6
M22898	M22898	Tumor protein p53 (Li-Fraumeni syndrome)	1.6
U90549	U90549	Human non-histone chromosomal protein (NHC) mRNA	1.6
J03934	J03934	NAD(P)H:menadione oxidoreductase	1.6
X53793	X53793	MULTIFUNCTIONAL PROTEIN ADE2	1.6
U76992	U76992	Human Tat-SF1 mRNA complete cds	1.6
U09820	U09820	X-LINKED HELICASE II	1.6
X58521	X58521	NUCLEAR PORE GLYCOPROTEIN P62	1.6
RC_AA121127	AA121127	ESTs Weakly similar to ZK1058.4 [C.elegans]	1.6
RC_AA243007	AA243007	ESTs	1.6
RC_AA463195	AA463195	ESTs	1.6
U90909	U90909	Human clone 23722 mRNA sequence	1.6
RC_W15528	W15528	ESTs	1.6
R70621	R70621	ESTs Highly similar to hypothetical protein 100K	1.6
RC_AA456598	AA456598	ESTs	1.6
RC_AA167375	AA167375	Homo sapiens mRNA for KIAA0530 protein partial cds	1.6
RC_AA279667	AA279667	Cathepsin B	1.6
RC_F03738_f	F03738	ESTs	1.6
RC_AA148885	AA148885	ESTs	1.6
RC_D60856_f	D60856	Homo sapiens UDP-glucose dehydrogenase (UGDH)	1.6

FIGURE 4 (CONT.)

		EST	1.6
RC_AA101811	AA101811	ESTs	1.6
RC_AA347967	AA347967		1.6
U05237	U05237	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA	1.6
RC_AA256678	AA256678	ESTs Highly similar to POP2 PROTEIN [Saccharomyces	1.6
X69910	X69910	H.sapiens p63 mRNA for transmembrane protein	1.6
RC_H95039	H95039	Homo sapiens KIAA0442 mRNA partial cds	1.6
RC_AA181580	AA181580	Homo sapiens importin beta subunit mRNA complete cds	1.6
RC_AA219699	AA219699	ESTs	1.5
RC_AA236672	AA236672	ESTs Weakly similar to DFS70 [H.sapiens]	1.5
RC_AA476319	AA476319	ESTs	1.5
RC_AA041551	AA041551	ESTs	1.5
AA195179_s	AA195179	ESTs	1.5
RC_AA256492	AA256492	ESTs	1.5
RC_W93640	W93640	ESTs	1.5
RC_R07016	R07016		1.5
RC_AA232644	AA232644	Protein tyrosine phosphatase non-receptor type 4	1.5
RC_N37065	N37065	ESTs	1.5
RC_T10258	T10258	EST	1.5
RC_AA279757	AA279757	ESTs Weakly similar to similar to mouse MMR1	1.5
RC_N67390	N67390	ESTs	1.5
RC_AA489086	AA489086	ESTs	1.5
RC_W72138	W72138	Homo sapiens putative transcriptional repressor E2F-6	1.5
RC_N68640	N68640	ESTs	1.5
RC_D51177	D51177	ESTs	1.5
RC_AA400271	AA400271	ESTs Highly similar to CALCIUM-TRANSPORTING	1.5
D85418	D85418	Human mRNA for phosphatidylinositol-glycan-class C	1.5
U41668	U41668	Deoxyguanosine kinase	1.5
RC_AA133309	AA133309	EST	1.5
AA113913	AA113913	EST - AA113913	1.5
RC_N21978	N21978	ESTs	1.5
RC_AA447970	AA447970	EST	1.5
RC_AA433925	AA433925	ESTs	1.5
D31764	D31764	Human mRNA for KIAA0064 gene complete cds	1.5
AA146888_s	AA146888	ESTs Highly similar to COATOMER ZETA SUBUNIT	1.5
W28366	W28366	Homo sapiens clone 24800 mRNA sequence	1.5
RC_AA293568	AA293568	ESTs	1.5
RC_N48677	N48677	ESTs	1.5
RC_AA226922	AA226922	ESTs Highly similar to CLATHRIN COAT ASSEMBLY	1.5
RC_N52271	N52271	Homo sapiens LIM protein mRNA complete cds	1.5
M31523	M31523	Transcription factor 3 (E2A immunoglobulin enhancer	1.5

FIGURE 4 (CONT.)

D38521	D38521	Human mRNA for KIAA0077 gene partial cds	1.5
M63167	M63167	V-akt murine thymoma viral oncogene homolog 1	1.5
HG884-HT884	TIGR - HG884-	EST - HG884-HT884	1.5
U50939	U50939	Human amyloid precursor protein-binding protein 1	1.5
U35451	U35451	Homo sapiens heterochromatin protein p25 mRNA	1.5
U94836	U94836	Human ERPROT 213-21 mRNA complete cds	1.5
L33881	L33881	Protein kinase C iota	1.5
L18960	L18960	Eukaryotic translation initiation factor 4C (eIF-4C)	1.5
RC_AA496257	AA496257	ESTs Weakly similar to DIPEPTIDYL PEPTIDASE IV	1.5
RC_AA262942	AA262942	ESTs	1.5
RC_AA056735	AA056735	ESTs Weakly similar to HYPOTHETICAL PROTEIN	1.5
RC_AA482014	AA482014	H.sapiens mRNA for centrin gene	1.5
U09564	U09564	Human serine kinase mRNA complete cds	1.5
RC_AA609738	AA609738	ESTs	1.5
RC_N54450_i	N54450	ESTs	1.5
RC_Z39255_f	Z39255	ESTs	1.5
RC_N78717_s	N78717	H.sapiens mRNA for translin	1.5
RC_R87660	R87660	EST - RC_R87660	1.5
RC_T98843	T98843	ESTs Moderately similar to !!!! ALU SUBFAMILY J	1.5
RC_Z39211	Z39211	Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP)	1.5
RC_AA412528	AA412528	ESTs Weakly similar to ORF2 consensus sequence	1.5
RC_N26101	N26101	ESTs Weakly similar to DPY-30 PROTEIN [C.elegans]	1.5
RC_AA399550	AA399550	ESTs	1.5
RC_AA621580	AA621580	ESTs Highly similar to HYPOTHETICAL 66.5 KD	1.5
AA422160	AA422160	H.sapiens NAP (nucleosome assembly protein) mRNA	1.4
RC_AA156542	AA156542	ESTs	1.4
H59417_s	H59417	ESTs	1.4
RC_AA460246	AA460246	ESTs Weakly similar to similar to tyrosyl-tRNA	1.4
RC_F04982	F04982	ESTs	1.4
AA285277	AA285277	Homo sapiens brain expressed ring finger protein mRNA	1.4
RC_R09196	R09196	ESTs Moderately similar to M-phase phosphoprotein 11	1.4
RC_F09983	F09983	ESTs	1.4
RC_AA057193	AA057193	ESTs	1.4
RC_AA449068	AA449068	ESTs	1.4
AA452724	AA452724	Homo sapiens TFAR19 mRNA complete cds	1.4
M29580	M29580	Zinc finger protein 7 (KOX 4 clone HF.16)	1.4
RC_AA417895	AA417895	ESTs	1.4
RC_AA425100	AA425100	ESTs	1.4
RC_AA287879	AA287879	ESTs Highly similar to GTP-BINDING PROTEIN SARA	1.4
RC_T17440_f	T17440	ESTs	1.4

FIGURE 4 (CONT.)

RC_AA255554	AA255554	ESTs	1.4
AA402937	AA402937	ESTs	1.4
RC_N92293	N92293	EST	1.4
RC_AA292128	AA292128	ESTs	1.4
RC_R01243	R01243	ESTs	1.4
U26727	U26727	Cyclin-dependent kinase inhibitor 2A (melanoma p16	1.4
D38498_f	D38498	Human PMS5 mRNA (yeast mismatch repair gene PMS1	1.4
M62810	M62810	Transcription factor 6-like 1 (mitochondrial transcription	1.4
RC_AA279991	AA279991	ESTs	1.4
RC_N66569	N66569	ESTs	1.4
RC_AA287138	AA287138	ESTs Weakly similar to ASPARTYL-TRNA	1.4
RC_AA278755	AA278755	ESTs Weakly similar to !!!! ALU SUBFAMILY SB1	1.4
RC_AA195515	AA195515	ESTs	1.4
RC_R63925	R63925	ESTs	1.4
RC_N23972	N23972	ESTs	1.4
RC_W93379_s	W93379	H.sapiens nek2 mRNA for protein kinase	1.4
L06419	L06419	Lysyl hydroxylase	1.4
RC_AA411882	AA411882	ESTs	1.4
RC_AA085918	AA085918	H.sapiens HUNKI mRNA	1.4
U12595	U12595	Human tumor necrosis factor type 1 receptor associated	1.4
RC_AA262943	AA262943	ESTs	1.4
RC_AA135095	AA135095	Homo sapiens Sox-like transcriptional factor mRNA	1.4
RC_T16226	T16226	ESTs	1.4
RC_AA497015	AA497015	Homo sapiens chromosome 19 cosmid R32469	1.4
RC_AA171939	AA171939	ESTs	1.4
AB004884	AB004884	Homo sapiens mRNA for PKU-alpha partial cds	1.4
U84720	U84720	Homo sapiens mRNA export protein (RAE1) mRNA	1.4
RC_Z40041	Z40041	ESTs	1.4
RC_W60473	W60473	ESTs	1.4
RC_Z38501	Z38501	ESTs Weakly similar to PROBABLE E5 PROTEIN	1.4
RC_H93708_s	H93708	CLEAVAGE SIGNAL-1 PROTEIN	1.4
RC_AA025086	AA025086	ESTs	1.4
RC_N64244	N64244	ESTs	1.4
U07418	U07418	DNA mismatch repair protein MLH1	1.4
RC_R64660	R64660	ESTs	1.4
RC_AA400093	AA400093	ESTs Weakly similar to HYPOTHETICAL 48.8 KD	1.4
RC_AA490949	AA490949	ESTs	1.4
RC_D80921_s	D80921	Homo sapiens clone 23965 mRNA sequence	1.4
RC_N26722	N26722	ESTs	1.4
RC_W90146_f	W90146	ESTs	1.4

FIGURE 4 (CONT.)

RC_AA114250	AA114250	Homo sapiens mRNA for KIAA0512 protein complete cds	1.4
RC_AA031357	AA031357	ESTs	1.3
T68510	T68510	ESTs	1.3
M95767	M95767	DI-N-ACETYLCHITOBIASE PRECURSOR	1.3
RC_W67524	W67524	Human protein-tyrosine phosphatase (HU-PP-1) mRNA	1.3
RC_AA465093	AA465093	ESTs	1.3
RC_H26417	H26417	ESTs	1.3
RC_T64438	T64438	ESTs Weakly similar to C01A2.4 [C.elegans]	1.3
RC_D11718	D11718	ESTs	1.3
RC_Z41963_r	Z41963	Homo sapiens HP protein (HP) mRNA complete cds	1.3
RC_AA252079	AA252079	Homo sapiens mRNA for dachshund protein	1.3
RC_AA262889	AA262889	ESTs	1.3
RC_AA487492	AA487492	Homo sapiens clone 23592 mRNA sequence	1.3
RC_AA464428	AA464428	ESTs	1.3
RC_H38828_s	H38828	H.sapiens RBQ-1 mRNA	1.3
RC_H71863_s	H71863	Zinc finger protein 139 (clone pHZ-37)	1.3
RC_AA040696	AA040696	ESTs	1.3
RC_AA258189	AA258189	ESTs	1.3
RC_AA443294	AA443294	Homo sapiens putative transcriptional repressor E2F-6	1.3
U66561	U66561	Human kruppel-related zinc finger protein (ZNF184)	1.3
X69398	X69398	CD47 antigen (Rh-related antigen integrin-associated	1.3
RC_AA122394	AA122394	ESTs	1.3
RC_T40707	T40707	ESTs	1.3
RC_AA435536	AA435536	ESTs	1.3
RC_AA206800	AA206800	ESTs Weakly similar to ZINC FINGER PROTEIN 135	1.3
RC_AA001386	AA001386	EST	1.3
RC_AA428992	AA428992	ESTs	1.3
RC_R49886	R49886	ESTs	1.3
RC_T95591	T95591	ESTs	1.3
RC_AA338760	AA338760	ESTs	1.3
RC_AA098864	AA098864	ESTs	1.3
AA234817	AA234817	ESTs	1.3
RC_AA059051	AA059051	ESTs	1.3
RC_AA046619	AA046619	ESTs	1.3
RC_AA461169	AA461169	ESTs	1.3
RC_AA449071	AA449071	ESTs	1.3
RC_N24732	N24732	ESTs	1.3
RC_AA400195	AA400195	ESTs	1.3
RC_AA029264	AA029264	ESTs	1.3
RC_W86978	W86978		

FIGURE 4 (CONT.)

RC_H38086	H38086	Human N-ethylmaleimide-sensitive factor mRNA partial	1.3
RC_F13663	F13663	ESTs	1.3
AA458542	AA458542		1.3
RC_AA101601	AA101601	Homo sapiens chromosome 19 cosmid R32469	1.3
RC_AA598675	AA598675	ESTs Highly similar to Polio virus receptor protein	1.3
AA156670_s	AA156670	ESTs	1.3
AA059415	AA059415		1.3
RC_AA485424	AA485424	Homo sapiens agrin precursor mRNA partial cds	1.3
M64929	M64929	ESTs Moderately similar to !!!! ALU SUBFAMILY SB	1.3
U28686	U28686	ESTs	1.3
U02680	U02680		1.3
U96113	U96113	Protein phosphatase 2 (formerly 2A) regulatory subunit B	1.3
X97544	X97544	Human putative RNA binding protein RNPL mRNA	1.3
Z46629	Z46629	Human protein tyrosine kinase mRNA complete cds	1.3
RC_H60061	H60061	EST - U96113	1.3
RC_AA007234	AA007234		1.3
AA329211_s	AA329211	H.sapiens mRNA for TIM17 preprotein translocase	1.3
RC_AA132007	AA132007	SRY (sex-determining region Y)-box 9 (campomelic	1.3
RC_AA417569	AA417569	ESTs Moderately similar to !!!! ALU SUBFAMILY SB	1.3
RC_AA236200	AA236200	ESTs	1.3
RC_AA126426	AA126426		1.3
RC_AA504499	AA504499	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-	1.3
RC_AA521471	AA521471	Down-regulator of transcription 1 TBP-binding (negative	1.3
RC_H83438_s	H83438	ESTs	1.3
RC_T23932_f	T23932	ESTs	1.3
RC_T59859	T59859		1.3
RC_N20630_i	N20630	Human brain secretory protein hSec10p (HSEC10) mRNA	1.3
D87466	D87466	ESTs Highly similar to probable chloride channel 3	1.3
AA083339	AA083339	ESTs	1.3
RC_AA598506	AA598506		1.3
RC_AA278650	AA278650	Homo sapiens mRNA for DDS1beta protein complete cds	1.3
RC_AA599718	AA599718	ESTs	1.3
RC_AA398243	AA398243	ESTs	1.3
RC_N51855	N51855		1.3
RC_W52065_f	W52065	Human mRNA for KIAA0276 gene partial cds	1.3
L38961	L38961	ESTs	1.3
RC_N55304_s	N55304		1.3
AA147543	AA147543	Human mRNA for KIAA0179 gene partial cds	1.3
RC_T32794_s	T32794	ESTs	1.3
U51698	U51698		1.3
		H.sapiens mRNA for translin associated protein X	1.3
		ESTs Highly similar to RSP5 PROTEIN [Saccharomyces	1.3
		ESTs Moderately similar to NAD(+) ADP-	1.3
		Homo sapiens mRNA for KIAA0539 protein complete cds	1.3
		Integral transmembrane protein 1	1.2
		ESTs	1.2
		ESTs	1.2
		ESTs	1.2
		ESTs	1.2

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FIGURE 4 (CONT.)

		ESTs	1.2
RC_AA464758	AA464758		1.2
X02751	X02751	Neuroblastoma RAS viral (v-ras) oncogene homolog	1.2
RC_W87544	W87544	ESTs	1.2
RC_AA025746	AA025746	ESTs	1.2
RC_R62444	R62444	ESTs	1.2
RC_H05635	H05635	ESTs Highly similar to 50S RIBOSOMAL PROTEIN L13	1.2
RC_AA433943	AA433943	ESTs Weakly similar to hnRNA-binding protein M4	1.2
N42440	N42440	ESTs	1.2
W03007	W03007	ESTs Weakly similar to !!!! ALU SUBFAMILY J	1.2
RC_T99364	T99364	Homo sapiens clone 23685 mRNA sequence	1.2
RC_AA411708	AA411708	CCAAT/enhancer binding protein (C/EBP) gamma	1.2
U20240	U20240	EST - AA112222	1.2
AA112222	AA112222	ESTs	1.2
RC_W61011	W61011	ESTs	1.2
RC_AA010188	AA010188	ESTs	1.2
RC_N67104	N67104	ESTs	1.2
RC_N71027	N71027	ESTs	1.2
RC_AA398222	AA398222	EST - RC_T85190	1.2
RC_T85190	T85190	ESTs	1.2
RC_N74635	N74635	ESTs	1.2
RC_Z38839	Z38839	Human endonuclease III homolog mRNA complete cds	1.2
U79718	U79718	ESTs	1.2
AA355201	AA355201	YY1 transcription factor	1.2
Z14077_s	Z14077	ESTs Highly similar to HYPOTHETICAL 27.5 KD	1.2
RC_N68622	N68622	ESTs	1.2
RC_T17498	T17498		

FIGURE 5

Affymetrix ID	Accession	Gene Name	Ratio tumor v. breast
RC_T79956	T79956	ESTs	135.3
RC_AA453638	AA453638	EST - RC_AA453638	107.3
RC_AA461322	AA461322	EST	81.8
RC_AA461510	AA461510	EST - RC_AA461510	75.3
RC_R67275_s	R67275	Collagen type XI alpha 1	72.9
RC_AA453518	AA453518	ESTs	61.5
RC_N27351	N27351	EST - RC_N27351	57.1
RC_AA486737	AA486737	H.sapiens mRNA for Sm protein F	53.9
RC_AA453479	AA453479	Human focal adhesion kinase (FAK) mRNA complete cds	53.2
RC_AA285050	AA285050	ESTs Weakly similar to zinc-finger protein Zn72D	52
RC_AA291468	AA291468	ESTs	46.8
RC_Z40805	Z40805	ESTs	45.7
RC_AA169440	AA169440	ESTs	38.9
D90041_s	D90041	ARYLAMINE N-ACETYLTRANSFERASE	33.6
RC_AA232294	AA232294	EST - RC_AA232294	32.6
RC_R86839	R86839	EST - RC_R86839	32.4
RC_AA453641	AA453641	EST	31.1
RC_AA609955	AA609955	EST	30.6
RC_AA283905	AA283905	ESTs	28.3
RC_AA211831	AA211831	EST - RC_AA211831	28.1
RC_AA412090	AA412090	ESTs	28
RC_N27159_s	N27159	Inhibin beta A (activin A activin AB alpha polypeptide)	25.5
RC_R65763	R65763	EST	23.9
RC_R97063	R97063	ESTs	22.8
RC_AA232940	AA232940	EST - RC_AA232940	21.7
RC_AA463189	AA463189	ESTs	20.9
RC_AA421171	AA421171	ESTs	19.5
RC_AA251875	AA251875	ESTs Moderately similar to POL POLYPROTEIN [Feline	19.4
RC_AA054228	AA054228	ESTs	17.7
RC_AA621462	AA621462	CARCINOEMBRYONIC ANTIGEN PRECURSOR	17.1
RC_AA505133	AA505133	ESTs	17.1
RC_AA488191	AA488191	ESTs	16.8
RC_AA211158	AA211158	EST - RC_AA211158	16.8
RC_AA481883	AA481883	ESTs	16.2
RC_AA196768	AA196768	ESTs	16.1
H83527_s	H83527	ESTs Highly similar to thyroid disease hypothetical	16.1

FIGURE 5 (CONT.)

RC_AA196721	AA196721	EST - RC_AA196721	16.1
RC_T25875	T25875	Homo sapiens clone 23967 unknown mRNA partial cds	15.8
X57579	X57579	Inhibin beta A (activin A activin AB alpha polypeptide)	15.8
RC_AA191404	AA191404	ESTs	15.2
RC_AA262969	AA262969	ESTs Weakly similar to B0334.4 [C.elegans]	14.9
RC_AA436611	AA436611	Human fibroblast activation protein mRNA complete cds	14.7
RC_R51309	R51309	ESTs	14.6
RC_AA461297	AA461297	ESTs	14.6
RC_AA430032	AA430032	ESTs Moderately similar to PTTG gene product	14.4
RC_AA280679	AA280679	ESTs	14.4
M81057	M81057	Carboxypeptidase B1 (tissue)	14.4
RC_R07976	R07976	ESTs Highly similar to HYPOTHETICAL 21.5 KD	14.3
RC_R46627	R46627	ESTs	14.2
RC_AA461559	AA461559	Chromogranin A (parathyroid secretory protein 1)	14.1
AA092129_f	AA092129	ESTs Moderately similar to 25E8.1 [D.melanogaster]	14
RC_AA436893	AA436893	ESTs Weakly similar to TH1 protein [D.melanogaster]	14
M23263	M23263	Androgen receptor (dihydrotestosterone receptor testicular	13.9
RC_AA486538	AA486538	ESTs Weakly similar to hypothetical protein 1 [H.sapiens]	13.9
RC_D20379	D20379	ESTs	13.7
RC_AA076138	AA076138	Homo sapiens histone macroH2A1.2 mRNA complete cds	13.5
RC_AA045074	AA045074	ESTs Weakly similar to 52-kD SS-A/Ro autoantigen	13.4
RC_D60354_s	D60354	Human mRNA for KIAA0007 gene partial cds	13.3
RC_T78922_s	T78922	Homo sapiens mRNA for SCGF-beta complete cds	13.3
AA401334	AA401334	ESTs	13.3
RC_AA431350	AA431350	ESTs Moderately similar to !!!! ALU SUBFAMILY SC	13.1
RC_AA412065	AA412065	EST - RC_AA412065	13.1
RC_R61740_f	R61740	Homo sapiens regulator of G-protein signalling 12	13
RC_R54950	R54950	ESTs	12.8
AA037285	AA037285	Homo sapiens mRNA for A+U-rich element RNA binding	12.5
RC_AA233796	AA233796	ESTs	12.5
RC_AA219305	AA219305	EST	12.4
RC_AA252245	AA252245	ESTs	12.4
RC_AA041276	AA041276	ESTs Weakly similar to !!!! ALU SUBFAMILY SX	12.3
RC_AA463874	AA463874	Homo sapiens ES/130 mRNA complete cds	12.3
RC_AA461528	AA461528	ESTs	12.2
RC_AA099404	AA099404	ESTs	12.2
RC_AA214305	AA214305	ESTs	12.1
AA220223	AA220223	Fibroblast growth factor receptor 2 (bacteria-expressed	12.1

FIGURE 5 (CONT.)

RC_AA478571	AA478571	Glutamine-fructose-6-phosphate transaminase	12.1
RC_AA253217	AA253217	ESTs	11.8
RC_AA470074	AA470074	ESTs	11.5
RC_AA236010	AA236010	ESTs	11.4
J03589	J03589	UBIQUITIN-LIKE PROTEIN GDX	11.4
RC_R22952_s	R22952	ESTs	11.3
RC_W56363	W56363	ESTs Weakly similar to extracellular protein [H.sapiens]	11.3
RC_AA179298	AA179298	Homo sapiens chromosome 9 P1 clone 11659	11.3
RC_AA449232	AA449232	EST	11.2
RC_AA281733	AA281733	ESTs	11
RC_AA452601	AA452601	EST	11
RC_AA035630	AA035630	Homo sapiens U4/U6 small nuclear ribonucleoprotein	10.9
RC_AA453630	AA453630	EST	10.7
RC_R40431	R40431	ESTs	10.6
RC_AA405098	AA405098	ESTs Weakly similar to MOESIN/EZRIN/RADIXIN	10.6
RC_AA599259	AA599259	Human splicesomal protein (SAP 61) mRNA complete cds	10.4
X62078	X62078	GANGLIOSIDE GM2 ACTIVATOR PRECURSOR	10.4
RC_AA253170	AA253170	EST	10.4
RC_AA470156	AA470156	ESTs Weakly similar to dynein 74K chain cytosolic	10.3
RC_AA281290	AA281290	ESTs Highly similar to ZINC FINGER PROTEIN 85	10.2
RC_AA449832	AA449832	ESTs	10.1
RC_AA427898	AA427898	ESTs Weakly similar to trabecular meshwork inducible	10
RC_AA609867	AA609867	ESTs Weakly similar to No definition line found	10
RC_R49198_i	R49198	H.sapiens DAP-3 mRNA	9.9
RC_AA112396	AA112396	ESTs	9.8
RC_AA207015	AA207015	ESTs	9.8
RC_R06986_f	R06986	ESTs	9.7
M34338	M34338	Spermidine synthase	9.7
RC_AA228030	AA228030	ESTs	9.7
RC_AA447982	AA447982	ESTs Weakly similar to R01H10.6 [C.elegans]	9.7
Z14982_rna1	Z14982	PROTEASOME COMPONENT C13 PRECURSOR	9.7
RC_T97341	T97341	EST - RC_T97341	9.6
RC_AA143190	AA143190	ESTs Highly similar to HYPOTHETICAL 23.1 KD	9.5
RC_AA282914	AA282914	ESTs	9.4
RC_N21678	N21678	ESTs	9.3
RC_AA262111	AA262111	ESTs	9.3
D14657	D14657	Human mRNA for KIAA0101 gene complete cds	9.2
RC_AA007344	AA007344	ESTs	9.2

FIGURE 5 (CONT.)

RC_W73140	W73140	ESTs Highly similar to TRYPSINOGEN ANIONIC	9.2
RC_T16308_f	T16308	ESTs	9.1
RC_AA447666	AA447666	Human CENP-F kinetochore protein mRNA complete cds	9.1
HG2981-	TIGR -	EST - HG2981-HT3127	9
RC_R38919_i	R38919	EST	9
M86757	M86757	S100 calcium-binding protein A7 (psoriasin 1)	8.9
X72755	X72755	H.sapiens Humig mRNA	8.8
RC_AA443342	AA443342	ESTs	8.7
RC_AA481281	AA481281	ESTs	8.7
RC_AA608723	AA608723	ESTs	8.6
RC_AA457018	AA457018	ESTs	8.5
RC_AA113011	AA113011	Human mRNA for KIAA0314 gene partial cds	8.5
RC_H96237_s	H96237	Collagen type XI alpha 1	8.5
RC_AA024835	AA024835	Homo sapiens Shab-related delayed-rectifier K+ channel	8.4
S85655	S85655	Prohibitin	8.4
RC_N99976	N99976	ESTs	8.4
RC_T65004	T65004	EST - RC_T65004	8.4
RC_N93197	N93197	ESTs	8.3
J05070	J05070	Matrix metalloproteinase 2 (gelatinase A collagenase type	8.2
RC_R40177	R40177	ESTs	8.1
RC_D60302	D60302	ESTs	8.1
RC_W93659	W93659	ESTs	8
RC_N69464	N69464	ESTs	7.9
RC_AA458882	AA458882	ESTs Weakly similar to LINE-1 REVERSE	7.9
RC_AA421750	AA421750	EST	7.9
RC_N33011_s	N33011	Replication protein A (E coli RecA homolog RAD51	7.9
RC_AA447574	AA447574	ESTs	7.9
RC_R47948_i	R47948	ESTs	7.9
RC_AA235009	AA235009	ESTs	7.9
RC_R01634	R01634	ESTs	7.9
RC_AA150182	AA150182	ESTs Weakly similar to HYPOTHETICAL 88.1 KD	7.8
RC_AA446486	AA446486	Homo sapiens Ran binding protein 2 (RanBP2alpha)	7.8
RC_AA342084	AA342084	EST - RC_AA342084	7.8
RC_AA609170	AA609170	EST	7.8
RC_N46435	N46435	EST - RC_N46435	7.8
RC_AA417213	AA417213	ESTs	7.8
RC_T88814	T88814	ESTs	7.7
RC_AA459389	AA459389	Homo sapiens mRNA for tyrosyl sulfotransferase-2	7.7

FIGURE 5 (CONT.)

RC_H99879	H99879	ESTs Highly similar to EPIDERMAL GROWTH	7.6
RC_T68871	T68871	ESTs	7.6
U19796	U19796	Human melanoma antigen p15 mRNA complete cds	7.6
HG2981-	TIGR -	EST - HG2981-HT3938	7.6
RC_AA446008	AA446008	EST	7.6
D13666	D13666	Homo sapiens mRNA for osteoblast specific factor 2 (OSF-	7.5
RC_AA454566	AA454566	Human mRNA for KIAA0170 gene complete cds	7.5
RC_AA476937	AA476937	ESTs	7.5
W01296	W01296	EST - W01296	7.5
RC_AA282074	AA282074	ESTs	7.5
X02530	X02530	Interferon (gamma)-induced cell line protein 10 from	7.4
RC_N67889	N67889	ESTs	7.4
RC_AA609309	AA609309	ESTs	7.4
RC_AA412477	AA412477	EST	7.4
RC_AA459392	AA459392	ESTs	7.4
RC_AA599042	AA599042	EST	7.4
RC_AA443794	AA443794	ESTs	7.3
RC_AA121315	AA121315	ESTs	7.2
RC_R65593_s	R65593	Homo sapiens mRNA for kynurenine 3-monooxygenase	7.2
RC_AA427950	AA427950	EST - RC_AA427950	7.2
RC_AA088458	AA088458	ESTs Weakly similar to !!!! ALU SUBFAMILY J	7.2
RC_N67239	N67239	ESTs	7.1
AA310967_s	AA310967	ESTs Weakly similar to T04A8.11 [C.elegans]	7.1
RC_AA236177	AA236177	ESTs	7.1
RC_AA282143	AA282143	H.sapiens mRNA for melanoma growth regulatory protein	7.1
RC_AA283003	AA283003	ESTs	7.1
RC_AA421158	AA421158	ESTs	7.1
RC_T10082_f	T10082	ESTs	7.1
RC_Z40345	Z40345	ESTs Weakly similar to T06D8.5 [C.elegans]	7
RC_AA310499	AA310499	ESTs	7
RC_N34686	N34686	Homo sapiens clone 23915 mRNA sequence	7
RC_N71704	N71704	ESTs	6.9
U48705_mal	U48705	Receptor protein-tyrosine kinase EDDR1	6.9
RC_AA419461	AA419461	ESTs	6.8
RC_AA411204	AA411204	ESTs	6.8
RC_AA346385	AA346385	ESTs Highly similar to putative hydrophobic domain in	6.8
RC_D51229_f	D51229	Human clone 23589 mRNA sequence	6.8
M11718	M11718	Collagen type V alpha	6.7

FIGURE 5 (CONT.)

RC_N50550	N50550	Homo sapiens mRNA for Efs1 complete cds	6.7
L27841	L27841	Human autoantigen pericentriol material 1 (PCM-1)	6.7
RC_T92935	T92935	ESTs	6.7
U30246	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter	6.7
RC_AA034069	AA034069	ESTs	6.7
U24169	U24169	Human JTV-1 (JTV-1) mRNA complete cds	6.7
RC_AA435849	AA435849	ESTs Moderately similar to unknown protein [H.sapiens]	6.7
RC_H99935_s	H99935	Interleukin 6 signal transducer (gp130 oncostatin M	6.7
RC_R51988	R51988	ESTs	6.6
RC_AA505141	AA505141	ESTs	6.6
AA236384	AA236384	ESTs Highly similar to COP1 REGULATORY PROTEIN	6.5
RC_AA431085	AA431085	EST	6.5
X54326	X54326	MULTIFUNCTIONAL AMINOACYL-TRNA	6.4
U89606	U89606	Human pyridoxal kinase mRNA complete cds	6.4
RC_AA195651	AA195651	EST	6.4
RC_AA430211	AA430211	ESTs	6.4
D81608	D81608	H.sapiens mRNA for RNA polymerase II subunit	6.3
L77701	L77701	Homo sapiens COX17 mRNA complete cds	6.3
RC_AA443658	AA443658	Homo sapiens lamin B receptor homolog TM7SF2	6.3
RC_AA024664	AA024664	Human NADH:ubiquinone oxidoreductase subunit B13	6.2
RC_AA279943	AA279943	ESTs	6.2
RC_AA098874	AA098874	ESTs	6.2
RC_AA412106	AA412106	ESTs	6.2
U40271	U40271	Protein-tyrosine kinase 7	6.2
L37747_s	L37747	LAMIN B1	6.1
U78525	U78525	Human eukaryotic translation initiation factor (eIF3)	6.1
RC_T77733_s	T77733	Tubulin gamma polypeptide	6.1
RC_D20280	D20280	ESTs	6.1
RC_W69807	W69807	ESTs Highly similar to GOLIATH PROTEIN [Drosophila	6.1
RC_AA133199	AA133199	ESTs	6.1
RC_H55748	H55748	ESTs	6.1
RC_AA479933	AA479933	ESTs	6.1
L32137	L32137	Human germline oligomeric matrix protein (COMP)	6.1
RC_AA448349	AA448349	ESTs	6.1
RC_AA600257	AA600257	ERGIC-53 PROTEIN PRECURSOR	6.1
RC_R99978	R99978	ESTs Weakly similar to line-1 protein ORF2 [H.sapiens]	6.1
J04177	J04177	Collagen type XI alpha 1	6
RC_AA406137	AA406137	EST	6

FIGURE 5 (CONT.)

U73514	U73514	Homo sapiens short chain L-3-hydroxyacyl-CoA	6
RC_W38407	W38407	ESTs	5.9
RC_AA292655	AA292655	ESTs	5.9
U65932	U65932	Human extracellular matrix protein 1 (ECM1) mRNA	5.8
RC_AA463740	AA463740	ESTs	5.8
M25753	M25753	Cyclin B1	5.8
RC_AA279292	AA279292	ESTs	5.8
RC_AA287665	AA287665	ESTs	5.8
RC_AA425379	AA425379	ESTs	5.8
RC_AA422007	AA422007	ESTs	5.8
HG2981-	TIGR -	EST - HG2981-HT3125	5.7
RC_R02572	R02572	Fibronectin 1	5.7
RC_AA442763	AA442763	ESTs Highly similar to G2/MITOTIC-SPECIFIC	5.7
RC_AA149624	AA149624	Homo sapiens mRNA for follistain-related protein (FRP)	5.7
RC_AA459945	AA459945	Homo sapiens mRNA for KIAA0585 protein partial cds	5.7
M34677	M34677	FACTOR VIII INTRON 22 PROTEIN	5.7
RC_AA454562	AA454562	ESTs	5.7
W30943	W30943	ESTs	5.7
RC_AA232956	AA232956	ESTs	5.6
U91327	U91327	EST - U91327	5.6
RC_AA453987	AA453987	ESTs	5.6
RC_AA040154	AA040154	ESTs	5.6
RC_T23528	T23528	ESTs Moderately similar to TYKi protein [M.musculus]	5.6
X76105	X76105	H.sapiens DAP-1 mRNA	5.6
RC_AA398212	AA398212	ESTs	5.6
RC_AA416986	AA416986	Guanine nucleotide binding protein (G protein) beta	5.6
RC_T95057_f	T95057	ESTs	5.6
U09278	U09278	Human fibroblast activation protein mRNA complete cds	5.5
RC_AA443602	AA443602	ESTs	5.5
RC_AA075200	AA075200	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-	5.5
X02874	X02874	(2'-5') oligoadenylate synthetase E	5.5
RC_R43883	R43883	ESTs	5.5
RC_T81310	T81310	EST	5.4
RC_H75933_i	H75933	Laminin receptor (2H5 epitope)	5.4
M97936	M97936	SIGNAL TRANSDUCER AND ACTIVATOR OF	5.4
RC_AA398721	AA398721	EST - RC_AA398721	5.4
RC_AA448410	AA448410	ESTs	5.4
RC_AA242757	AA242757	ESTs	5.4

FIGURE 5 (CONT.)

RC_AA479348	AA479348	H.sapiens mRNA for SYT	5.4
X03363	X03363	ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE	5.3
U59877	U59877	Human low-Mr GTP-binding protein (RAB31) mRNA	5.3
RC_N94385_s	N94385	Human germline oligomeric matrix protein (COMP)	5.3
RC_AA287022	AA287022	Thymidine kinase 1 soluble	5.3
RC_AA464860	AA464860	Homo sapiens Jak2 kinase mRNA complete cds	5.3
RC_AA488280	AA488280	EST - RC_AA488280	5.2
RC_AA403116	AA403116	Homo sapiens U-snRNP-associated cyclophilin (USA-	5.2
RC_H96392	H96392	ESTs	5.2
RC_W59961_s	W59961	Human mRNA for KIAA0389 gene complete cds	5.1
RC_AA487449	AA487449	EST - RC_AA487449	5.1
RC_R43543	R43543	ESTs	5.1
J05614	J05614	EST - J05614	5
RC_AA262179	AA262179	ESTs	5
RC_AA281451	AA281451	ESTs	5
RC_AA425691	AA425691	ESTs	5
RC_AA426376	AA426376	ESTs	5
RC_AA446000	AA446000	ESTs	5
AA479995	AA479995	Homo sapiens mRNA for KIAA0583 protein partial cds	5
RC_AA055892	AA055892	ESTs	5
RC_AA172056	AA172056	ESTs	5
C01169	C01169	Homo sapiens clone 23915 mRNA sequence	4.9
AA075599	AA075599	ESTs Highly similar to NADH-UBIQUINONE	4.7
RC_AA026356	AA026356	ESTs	4.7
X17059	X17059	ARYLAMINE N-ACETYLTRANSFERASE	4.6
U18321	U18321	H.sapiens DAP-3 mRNA	4.6
X57766	X57766	Human stromelysin-3 mRNA	4.5
RC_AA464853	AA464853	ESTs Weakly similar to T01G9.4 [C.elegans]	4.5
RC_AA227900	AA227900	H.sapiens mRNA homologous to S. cerevisiae RAD54	4.4
AA422025_s	AA422025	ESTs	4.4
RC_AA346495	AA346495	ESTs Moderately similar to !!!! ALU SUBFAMILY J	4.4
U73379	U73379	Human cyclin-selective ubiquitin carrier protein mRNA	4.3
U24389	U24389	Human lysyl oxidase-like protein mRNA complete cds	4.3
U21090	U21090	Human DNA polymerase delta small subunit mRNA	4.3
RC_H25577	H25577	ESTs Highly similar to CYTOCHROME P450 IVB1	4.2
S74445	S74445	Cellular retinoic acid-binding protein [human skin mRNA	4.2
RC_AA419200	AA419200	ESTs	4.2
AA193297	AA193297	ESTs	4

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FIGURE 5 (CONT.)

U29463	U29463	Cytochrome B561	4
RC_R44709	R44709	Homo sapiens mRNA for RB18A protein	3.9
RC_AA459960	AA459960	ESTs Weakly similar to D9481.16 gene product	3.8
M25077	M25077	Human 60-kdal ribonucleoprotein (Ro) mRNA complete	3.7
RC_AA521240	AA521240	ESTs	3.6
RC_N63823	N63823	ESTs	3.6
RC_AA034365	AA034365	NUCLEAR PORE GLYCOPROTEIN P62	3.5
R70167	R70167	ESTs	3.5
L47276	L47276	EST - L47276	3.4
RC_AA442070	AA442070	Phosphoribosyl pyrophosphate amidotransferase	3.4
RC_AA116036	AA116036	ESTs	3.3
RC_R24237_f	R24237	ESTs	3.3
AD000092_cds	AD000092	Homo sapiens DNA from chromosome 19p13.2 cosmids	3.3
M86852	M86852	Peroxisomal membrane protein 3 (35kD Zellweger	3.2
RC_AA232939	AA232939	ESTs	3.2
X59798	X59798	Cyclin D1 (PRAD1 parathyroid adenomatosis 1)	3.1
RC_W44928	W44928	ESTs	3.1
RC_AA401687	AA401687	Homo sapiens ribonuclease P protein subunit p20 (RPP20)	3.1
RC_AA423827	AA423827	ESTs	3
RC_N32333	N32333	Homo sapiens M962 protein spliced isoform 2 mRNA	2.9
D00596	D00596	Thymidylate synthase	2.9
RC_AA399164	AA399164	ESTs	2.9
RC_AA164293	AA164293	ESTs	2.9
AA203523	AA203523	ESTs Weakly similar to coded for by C. elegans cDNA	2.9
RC_AA195936	AA195936	ESTs Weakly similar to W02D9.2 [C.elegans]	2.9
RC_AA485214	AA485214	DNA-BINDING PROTEIN NEFA PRECURSOR	2.9
RC_R50840	R50840	H.sapiens mRNA for ras-related GTP-binding protein	2.9
RC_R97040	R97040	ESTs	2.9
RC_N21159	N21159	Homo sapiens forkhead protein (FKHRL1) mRNA	2.8
RC_AA292765	AA292765	H.sapiens mRNA for M-phase phosphoprotein mpp5	2.8
RC_AA480103	AA480103	ESTs Weakly similar to !!!! ALU SUBFAMILY J	2.8
RC_AA412497	AA412497	EST	2.8
RC_H24460_s	H24460	FK506-binding protein 4 (59kD)	2.8
RC_R39234_r	R39234	ESTs Weakly similar to elastin like protein	2.8
RC_R79617	R79617	ESTs	2.8
U33052	U33052	Human lipid-activated protein kinase PRK2 mRNA	2.7
D63391	D63391	Human mRNA for platelet activating factor	2.7
RC_W69160	W69160	ESTs	2.7

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FIGURE 5 (CONT.)

RC_F02863	F02863	ESTs Moderately similar to !!!! ALU SUBFAMILY SQ	2.7
L11669	L11669	Human tetracycline transporter-like protein mRNA	2.7
M96982	M96982	SPLICING FACTOR U2AF 35 KD SUBUNIT	2.7
Z49099	Z49099	H.sapiens mRNA for spermine synthase	2.6
RC_AA598648	AA598648	Human mRNA for transcriptional activator hSNF2b	2.6
RC_AA447617	AA447617	ESTs	2.6
RC_N92948_s	N92948	Human IEF SSP 9502 mRNA complete cds	2.6
RC_AA130349	AA130349	ESTs	2.5
AB002308	AB002308	Human mRNA for KIAA0310 gene complete cds	2.5
L00205	L00205	KERATIN TYPE II CYTOSKELETAL 6D	2.5
RC_AA449458	AA449458	ESTs	2.4
RC_AA599674	AA599674	ESTs Weakly similar to F08G12.1 [C.elegans]	2.4
R81830	R81830	Homo sapiens breast cancer putative transcription factor	2.3
RC_N49284_s	N49284	MYB PROTO-ONCOGENE PROTEIN	2.3
RC_AA069285	AA069285	ESTs Weakly similar to PROBABLE UBIQUITIN	2.3
RC_N33063	N33063	ESTs Highly similar to GAG POLYPROTEIN [Avian	2.3
RC_AA250737	AA250737	ESTs	2.3
U77180	U77180	Human mRNA for EBI1-ligand chemokine complete cds	2.3
RC_AA028028	AA028028	ESTs	2.2
RC_AA485223	AA485223	ESTs	2.2
RC_AA148516	AA148516	ESTs	2.2
X70683	X70683	SRY (sex determining region Y)-box 4	2.1
RC_AA609869	AA609869	ESTs	2.1
RC_W20391_s	W20391	Human mRNA for kinesin-related protein partial cds	2.1
M23263	M23263	Androgen receptor (dihydrotestosterone receptor testicular	2
RC_AA487202	AA487202	ESTs	2
RC_F02651	F02651	ESTs	2
RC_AA476582	AA476582	ESTs Highly similar to SIGNAL RECOGNITION	2
RC_W80467	W80467	ESTs	2
U37519	U37519	Aldehyde dehydrogenase 8	2
W28362	W28362	ESTs	2
RC_AA045481	AA045481	ESTs	2
AA443460	AA443460	ESTs	2
U76638	U76638	Human BRCA1-associated RING domain protein	1.9
RC_W80763	W80763	ESTs Highly similar to FK506-BINDING PROTEIN	1.9
AA464013	AA464013	ESTs Weakly similar to Y53C12A.3 [C.elegans]	1.9
RC_AA599219	AA599219	ESTs Moderately similar to ALR [H.sapiens]	1.8
RC_Z40332	Z40332	Homo sapiens mRNA for p115 complete cds	1.8

FIGURE 5 (CONT.)

RC_AA056588	AA056588	ESTs	1.7
D78151	D78151	H.sapiens mRNA for 55.11 binding protein	1.7
RC_AA287091	AA287091	ESTs Highly similar to C10 [H.sapiens]	1.7
D50840	D50840	Human mRNA for ceramide glucosyltransferase complete	1.6
RC_AA456437	AA456437	ESTs Weakly similar to CLEAVAGE STIMULATION	1.6
RC_AA026418	AA026418	ESTs	1.6
RC_AA293568	AA293568	ESTs	1.5
RC_AA279757	AA279757	ESTs Weakly similar to similar to mouse MMR1	1.5
RC_AA085918	AA085918	H.sapiens HUNK1 mRNA	1.4
RC_AA156542	AA156542	ESTs	1.4
U12595	U12595	Human tumor necrosis factor type 1 receptor associated	1.4
RC_AA262943	AA262943	ESTs	1.4
RC_T16226	T16226	ESTs	1.4
RC_AA057193	AA057193	ESTs	1.4
RC_AA171939	AA171939	ESTs	1.4
RC_AA101601	AA101601	ESTs Highly similar to Polio virus receptor protein	1.3
M95767	M95767	DI-N-ACETYLCHITOBIASE PRECURSOR	1.3
RC_AA487492	AA487492	Homo sapiens clone 23592 mRNA sequence	1.3
AA156670_s	AA156670	Homo sapiens agrin precursor mRNA partial cds	1.3
RC_AA040696	AA040696	ESTs	1.3
L38961	L38961	Integral transmembrane protein 1	1.2
U51698	U51698	ESTs	1.2

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FIGURE 6

Affymetrix ID	Accession	Gene Name	ratio tumor vs breast	Associated with chromosomal gain (by CGH)?
RC_T79956	T79956	ESTs	135.3	
RC_AA453638	AA453638	EST - RC_AA453638	107.3	
RC_AA461322	AA461322	EST	81.8	
RC_AA461510	AA461510	EST - RC_AA461510	75.3	
RC_R67275_s	R67275	Collagen type XI alpha 1	72.9	
RC_AA453518	AA453518	ESTs	61.5	
RC_N27351	N27351	EST - RC_N27351	57.1	
RC_AA486737	AA486737	H sapiens mRNA for Sm protein F	53.9	
RC_AA453479_s	AA453479	Human focal adhesion kinase (FAK) mRNA complete cds	53.2	YES
RC_AA285050_s	AA285050	ESTs Weakly similar to zinc-finger protein Zn72D [D.melanogaster]	52	
RC_AA291468	AA291468	ESTs	46.8	
RC_Z40805	Z40805	ESTs	45.7	
RC_AA169440	AA169440	ESTs	38.9	
RC_AA453641	AA453641	EST	31.1	
RC_AA609955	AA609955	EST	30.6	
RC_AA283905	AA283905	ESTs	28.3	
RC_AA412090	AA412090	ESTs	28	
RC_N27159_s	N27159	Inhibin beta A (activin A activin AB alpha polypeptide)	25.5	
RC_R65763	R65763	EST	23.9	
RC_R97063	R97063	ESTs	22.8	
RC_AA463189	AA463189	ESTs	20.9	
RC_AA505133	AA505133	ESTs	17.1	
H83527_s	H83527	ESTs Highly similar to thyroid disease hypothetical autoantigen [H.sapiens]	16.1	
RC_AA196768_s	AA196768	ESTs	16.1	
X57579	X57579	Inhibin beta A (activin A activin AB alpha polypeptide)	15.8	YES
RC_AA191404	AA191404	ESTs	15.2	
RC_AA262969_f	AA262969	ESTs Weakly similar to B0334.4 [C.elegans]	14.9	
RC_AA436611_s	AA436611	Human fibroblast activation protein mRNA complete cds	14.7	
M86757	M86757	S100 calcium-binding protein A7 (psoriasin 1)	8.9	
X72755	X72755	H sapiens Humig mRNA	8.8	
U19796	U19796	Human melanoma antigen p15 mRNA complete cds	7.6	
D13666	D13666	Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)	7.5	
X02530	X02530	Interferon (gamma)-induced cell line protein 10 from	7.4	
U48705_rna1	U48705	Receptor protein-tyrosine kinase EDDR1	6.9	
RC_AA346385	AA346385	ESTs Highly similar to putative hydrophobic domain in amino acid positions 373	6.8	
L32137	L32137	Human germline oligomeric matrix protein (COMP) mRNA complete cds	6.1	

FIGURE 6 (CONT.)

AA422025_s	AA422025	ESTs	4.4	YES
RC_H25577	H25577	ESTs Highly similar to CYTOCHROME P450 IVB1 [Oryctolagus cuniculus]	4.2	YES
RC_T15916	T15916	ESTs Highly similar to COATOMER GAMMA SUBUNIT [Saccharomyces cere	3.2	YES
AA203523	AA203523	ESTs Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]	2.9	YES
RC_R50840	R50840	H.sapiens mRNA for ras-related GTP-binding protein	2.9	YES
RC_H24460_s	H24460	FK506-binding protein 4 (59kD)	2.8	YES
RC_AA125969	AA125969	ESTs Weakly similar to F35G12.9 [C.elegans]	2.7	YES
RC_AA293300_s	AA293300	ESTs Weakly similar to semaphorin C [M.musculus]	2.6	YES
RC_AA447617	AA447617	ESTs	2.6	YES
RC_R50333_i	R50333	ESTs	2.6	YES
X55448_cds1	X55448	Glucose-6-phosphate dehydrogenase	1.9	YES
RC_AA443962	AA443962	ESTs Weakly similar to monocytic leukaemia zinc finger protein [H.sapiens]	1.8	YES
RC_AA293568	AA293568	ESTs	1.5	YES
RC_D20342_i	D20342	Human mRNA for Tob complete cds	1.2	YES

Affymetrix ID	Accession	Gene Name	ratio tumor vs breast	ORF structural info
RC_T79956	T79956	ESTs	135.3	?
RC_AA453640	AA453640	ESTs	121.4	other
RC_AA453638	AA453638	EST - RC_AA453638	107 3	?
RC_AA461322	AA461322	EST	81.8	?
RC_AA461510	AA461510	EST - RC_AA461510	75.3	other
RC_R67275_s	R67275	Collagen type XI alpha 1	72.9	other
RC_AA453518	AA453518	ESTs	61.5	other
RC_N27351	N27351	EST - RC_N27351	57.1	?
RC_AA486737	AA486737	H sapiens mRNA for Sm protein F	53.9	TM
RC_AA453479_s	AA453479	Human focal adhesion kinase (FAK) mRNA complete cds	53.2	other
RC_AA285050_s	AA285050	ESTs Weakly similar to zinc-finger protein Zn72D [D.melanogaster]	52	other
RC_AA291468	AA291468	ESTs	46.8	TM
RC_Z40805	Z40805	ESTs	45.7	other
RC_AA169440	AA169440	ESTs	38.9	other
D90041_s	D90041	ARYLAMINE N-ACETYLTRANSFERASE MONOMORPHIC	33.6	?
RC_AA621202	AA621202	ESTs	33.5	other
RC_AA232294	AA232294	EST - RC_AA232294	32.6	other
RC_R86839	R86839	EST - RC_R86839	32 4	other
S70585_ma1	S70585	GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR	31.3	?
RC_AA453641	AA453641	EST	31 1	SS.
RC_AA609955	AA609955	EST	30.6	TM
RC_AA283905	AA283905	ESTs	28.3	?
RC_AA211831	AA211831	EST - RC_AA211831	28 1	TM
RC_AA412090	AA412090	ESTs	28	other
RC_AA421289	AA421289	ESTs Weakly similar to ZINC FINGER PROTEIN MFG1 [Mus musculus]	25.5	other
RC_N27159_s	N27159	Inhibin beta A (activin A activin AB alpha polypeptide)	25 5	other
RC_T16687	T16687	ESTs	25.1	other
RC_R65763	R65763	EST	23.9	?
RC_AA487987	AA487987	EST	23.8	TM
RC_H99309	H99309	Human TFIID subunits TAF20 and TAF15 mRNA complete cds	23 6	other
RC_R97063	R97063	ESTs	22.8	other
RC_AA232940	AA232940	EST - RC_AA232940	21.7	other
RC_AA463189	AA463189	ESTs	20.9	TM
RC_AA421171	AA421171	ESTs	19 5	other
RC_AA251875_f	AA251875	ESTs Moderately similar to POL POLYPROTEIN [Feline endogenous virus ece1]	19 4	other
RC_AA054228	AA054228	ESTs	17 7	other
RC_D51215_f	D51215	EST - RC_D51215_f	17 4	other
RC_AA505133	AA505133	ESTs	17 1	other
RC_AA621462	AA621462	CARCINOEMBRYONIC ANTIGEN PRECURSOR	17 1	other
RC_AA232508	AA232508	ESTs	17	other
RC_AA024659_f	AA024659	H sapiens mRNA for hHKb1 protein	16 9	other
RC_AA211158	AA211158	EST - RC_AA211158	16 8	other
RC_AA488191	AA488191	ESTs	16 8	other
RC_AA290674_s	AA290674	Human 4E-binding protein 1 mRNA complete cds	16.3	other
RC_AA481883	AA481883	ESTs	16 2	TM
RC_AA196721	AA196721	EST - RC_AA196721	16 1	other
RC_AA196768_s	AA196768	ESTs	.16 1	other
H83527_s	H83527	ESTs Highly similar to thyroid disease hypothetical autoantigen [H sapiens]	16 1	other
RC_D51172	D51172	ESTs	15 9	other
RC_T25875	T25875	Homo sapiens clone 23967 unknown mRNA partial cds	15 8	other
X57579	X57579	Inhibin beta A (activin A activin AB alpha polypeptide)	15 8	?
J05068	J05068	TRANSCOBALAMIN I PRECURSOR	15.7	SS.
RC_AA487233	AA487233	ESTs Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H sapiens]	15 6	TM
RC_AA479969	AA479969	ESTs	15 4	other
RC_AA191404	AA191404	ESTs	15 2	other
RC_AA262969_f	AA262969	ESTs Weakly similar to B0334.4 [C elegans]	14 9	?
RC_AA436611_s	AA436611	Human fibroblast activation protein mRNA complete cds	14 7	SS.
RC_AA250843_s	AA250843	Interferon regulatory factor 5	14 6	?
RC_AA461297	AA461297	ESTs	14 6	other
RC_R51309	R51309	ESTs	14 6	other
RC_AA280679	AA280679	ESTs	14 4	?
RC_AA412029	AA412029	ESTs	14 4	other
RC_AA430032	AA430032	ESTs Moderately similar to PTTG gene product [R norvegicus]	14 4	?

FIGURE 7

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M81057	M81057	Carboxypeptidase B1 (tissue)	14 4	SS.
RC_R07976	R07976	ESTs Highly similar to HYPOTHETICAL 21.5 KD PROTEIN C08B11 9 IN CHROMOSOME II [Caenorhabditis elegans]	14 3	?
U75285_ma1	U75285	Human effector cell protease receptor-1 (EPR-1) gene partial cds	14 3	?
RC_R46627	R46627	ESTs	14 2	other
RC_AA461559	AA461559	Chromogranin A (parathyroid secretory protein 1)	14 1	?
AA092129_f	AA092129	ESTs Moderately similar to 25E8.1 [D melanogaster]	14	other
RC_AA436893	AA436893	ESTs Weakly similar to TH1 protein [D.melanogaster]	14	?
RC_AA465345	AA465345	ESTs	13 9	other
RC_AA486538	AA486538	ESTs Weakly similar to hypothetical protein 1 [H.sapiens]	13.9	other
M23263	M23263	Androgen receptor (dihydrotestosterone receptor testicular feminization spinal and bulbar muscular atrophy Kennedy disease)	13.9	TM
RC_D20379	D20379	ESTs	13.7	other
RC_AA076138	AA076138	Homo sapiens histone macroH2A1.2 mRNA complete cds	13.5	other
RC_W60486	W60486	ESTs Moderately similar to T11G6.8 [C.elegans]	13.5	other
RC_AA032243	AA032243	EST - RC_AA032243	13 4	other
RC_AA045074_s	AA045074	ESTs Weakly similar to 52-kD SS-A/Ro autoantigen [H sapiens]	13 4	other
RC_F01444_f	F01444	Homo sapiens KIAA0440 mRNA partial cds	13 4	other
AA401334	AA401334	ESTs	13.3	other
RC_D60354_s	D60354	Human mRNA for KIAA0007 gene partial cds	13.3	other
RC_T78922_s	T78922	Homo sapiens mRNA for SCGF-beta complete cds	13.3	other
RC_AA406635	AA406635	ESTs	13.1	other
RC_AA412065	AA412065	EST - RC_AA412065	13.1	other
RC_AA431350	AA431350	ESTs Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]	13.1	other
RC_AA431738	AA431738	EST	13 1	?
RC_R61740_f	R61740	Homo sapiens regulator of G-protein signalling 12 (RGS12) mRNA complete cds	13	other
RC_R54950	R54950	ESTs	12 8	other
RC_AA405488	AA405488	ESTs	12.7	TM
RC_AA418749	AA418749	EST	12 7	other
AA037285	AA037285	Homo sapiens mRNA for A+U-rich element RNA binding factor complete cds	12.5	other
RC_AA233796	AA233796	ESTs	12 5	other
RC_AA219305	AA219305	EST	12.4	?
RC_AA252245	AA252245	ESTs	12.4	TM
RC_AA041276	AA041276	ESTs Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H sapiens]	12.3	?
RC_AA463874	AA463874	Homo sapiens ES/130 mRNA complete cds	12.3	TM
RC_AA099404_s	AA099404	ESTs	12.2	other
RC_AA443985	AA443985	ESTs	12.2	?
RC_AA461528	AA461528	ESTs	12.2	TM
RC_AA214305	AA214305	ESTs	12.1	other
AA220223	AA220223	Fibroblast growth factor receptor 2 (bacteria-expressed kinase keratinocyte growth factor receptor craniofacial dysostosis 1 Crouzon syndrome Pfeiffer syndrome Jackson-Weiss syndrome)	12.1	SS,TM
RC_AA478571	AA478571	Glutamine-fructose-6-phosphate transaminase	12 1	TM
U31875	U31875	Human Hep27 protein mRNA complete cds	12 1	TM
RC_AA253217	AA253217	ESTs	11 8	other
RC_AA470074	AA470074	ESTs	11 5	other
RC_AA236010	AA236010	ESTs	11 4	other
RC_AA430002	AA430002	ESTs	11 4	other
D82307	D82307	ESTs Weakly similar to TH1 protein [D.melanogaster]	11.4	other
J03589	J03589	UBIQUITIN-LIKE PROTEIN GDX	11.4	?
RC_AA179298	AA179298	Homo sapiens chromosome 9 P1 clone 11659	11 3	other
RC_R22952_s	R22952	ESTs	11 3	?
RC_W56363	W56363	ESTs Weakly similar to extracellular protein [H sapiens]	11 3	TM
RC_AA449232	AA449232	EST	11 2	?
RC_AA444054	AA444054	ESTs Weakly similar to transmembrane protein [H sapiens]	11 1	?
RC_AA281733	AA281733	ESTs	11	other
RC_AA452601	AA452601	EST	11	?
RC_AA035630	AA035630	Homo sapiens U4/U6 small nuclear ribonucleoprotein hPrp4 mRNA complete cds	10 9	other
RC_AA235117	AA235117	ESTs Weakly similar to espin [R norvegicus]	10 9	other
RC_AA279418	AA279418	ESTs	10 9	TM
RC_AA432069	AA432069	ESTs	10 8	?
RC_AA453630	AA453630	EST	10 7	?
RC_W44657	W44657	EST	10 7	?
RC_AA405098	AA405098	ESTs Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D melanogaster]	10 6	other
RC_R40431	R40431	ESTs	10 6	other
RC_AA411425	AA411425	ESTs	10 5	other

FIGURE 7 (cont.)

RC_AA423956	AA423956	ESTs	10.5	other
RC_AA253170	AA253170	EST	10.4	?
RC_AA459347	AA459347	ESTs	10.4	other
RC_AA599259_s	AA599259	Human splicosomal protein (SAP 61) mRNA complete cds	10.4	other
X62078	X62078	GANGLIOSIDE GM2 ACTIVATOR PRECURSOR	10.4	SS.
RC_AA251430	AA251430	ESTs Highly similar to RAS-RELATED PROTEIN RAB-10 [Canis familiaris]	10.3	other
RC_AA470156	AA470156	ESTs Weakly similar to dynein 74K chain cytosolic [R.norvegicus]	10.3	SS.
RC_T64933_f	T64933	ESTs	10.3	other
RC_AA280609	AA280609	ESTs Weakly similar to K02B2.3 gene product [C.elegans]	10.2	other
RC_AA281290	AA281290	ESTs Highly similar to ZINC FINGER PROTEIN 85 [Homo sapiens]	10.2	?
RC_AA449832	AA449832	ESTs	10.1	other
RC_AA427898	AA427898	ESTs Weakly similar to trabecular meshwork inducible glucocorticoid response protein [H.sapiens]	10	other
RC_AA509867	AA509867	ESTs Weakly similar to No definition line found [C.elegans]	10	other
RC_AA465158	AA465158	EST	9.9	?
RC_R49198_i	R49198	H.sapiens DAP-3 mRNA	9.9	?
RC_AA112396	AA112396	ESTs	9.8	other
RC_AA207015	AA207015	ESTs	9.8	other
RC_AA228030	AA228030	ESTs	9.7	TM
RC_AA447982	AA447982	ESTs Weakly similar to R01H10.6 [C.elegans]	9.7	other
M34338	M34338	Spermidine synthase	9.7	other
RC_R06986_f	R06986	ESTs	9.7	?
Z14982_ma1	Z14982	PROTEASOME COMPONENT C13 PRECURSOR	9.7	?
RC_AA176247	AA176247	EST	9.6	other
RC_T97341	T97341	EST - RC_T97341	9.6	?
W26392	W26392	ESTs Highly similar to OVOSTATIN PRECURSOR [Gallus gallus]	9.6	other
RC_AA143190_s	AA143190	ESTs Highly similar to HYPOTHETICAL 23.1 KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]	9.5	TM
RC_AA452578	AA452578	ESTs	9.5	other
RC_AA258057	AA258057	ESTs	9.4	other
RC_AA282914	AA282914	ESTs	9.4	other
RC_AA461476	AA461476	ESTs Highly similar to PUTATIVE ATP-DEPENDENT RNA HELICASE C31A2 07C [Schizosaccharomyces pombe]	9.4	other
RC_W87751	W87751	ESTs	9.4	other
RC_W92713	W92713	ESTs	9.4	other
RC_AA262111	AA262111	ESTs	9.3	other
RC_AA490929	AA490929	EST	9.3	?
RC_N21678	N21678	ESTs	9.3	?
RC_N70690	N70690	ESTs	9.3	other
RC_N80716	N80716	ESTs	9.3	other
RC_AA007344	AA007344	ESTs	9.2	other
D14657	D14657	Human mRNA for KIAA0101 gene complete cds	9.2	other
RC_W73140	W73140	ESTs Highly similar to TRYPSINOGEN ANIONIC PRECURSOR [Canis familiaris]	9.2	other
RC_AA243020	AA243020	H.sapiens mRNA for disintegrin-metalloprotease (partial)	9.1	SS,TM
RC_AA431478	AA431478	ESTs	9.1	other
RC_AA447666_s	AA447666	Human CENP-F kinetochore protein mRNA complete cds	9.1	other
RC_T16308_f	T16308	ESTs	9.1	other
RC_R38919_i	R38919	EST	9	other
RC_R60223_s	R60223	ESTs	9	other
RC_R70379_s	R70379	Human germline IgD chain gene C-region C-delta-1 domain	9	?
HG2981-HT3127	TIGR - HG2981-HT3127	EST - HG2981-HT3127	9	?
M86757	M86757	S100 calcium-binding protein A7 (psoriasin 1)	8.9	SS,TM
RC_AA347209_s	AA347209	Human mRNA for KIAA0324 gene partial cds	8.8	other
RC_AA485041	AA485041	ESTs	8.8	other
X72755	X72755	H sapiens Humig mRNA	8.8	TM
RC_AA443342_s	AA443342	ESTs	8.7	other
RC_AA481281	AA481281	ESTs	8.7	other
RC_T96361_s	T96361	MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE	8.7	other
RC_AA608723	AA608723	ESTs	8.6	other
RC_H18027_s	H18027	Homo sapiens clone 23785 mRNA sequence	8.6	SS.
M86752	M86752	TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521	8.6	other
RC_AA113011_s	AA113011	Human mRNA for KIAA0314 gene partial cds	8.5	other
RC_AA457018	AA457018	ESTs	8.5	SS.
RC_H96237_s	H96237	Collagen type XI alpha 1	8.5	other
RC_AA024835	AA024835	Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA complete cds	8.4	TM

FIGURE 7 (cont.)

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RC_N99976	N99976	ESTs	8.4	other
S85655	S85655	Prohibitin	8.4	other
RC_T65004	T65004	EST - RC_T65004	8.4	other
RC_AA489510_s	AA489510	Homo sapiens clone 23716 mRNA sequence	8.3	?
RC_H72948_s	H72948	ESTs Highly similar to BONE/CARTILAGE PROTEOGLYCAN I (Bos taurus)	8.3	SS.
RC_N93197	N93197	ESTs	8.3	other
RC_Z39971_s	Z39971	ESTs	8.3	other
RC_AA236037	AA236037	ESTs Highly similar to HYPOTHETICAL 37.6 KD PROTEIN B0285.4 IN CHROMOSOME III (Caenorhabditis elegans)	8.2	?
J05070	J05070	Matrix metalloproteinase 2 (gelatinase A, collagenase type IV)	8.2	TM
RC_AA419225	AA419225	Human mariner-like element-containing mRNA clone pcHMT1	8.1	other
RC_D60302	D60302	ESTs	8.1	other
RC_H98621_s	H98621	Homo sapiens mRNA for KIAA0617 protein, complete cds	8.1	?
RC_R40177	R40177	ESTs	8.1	other
RC_AA233545	AA233545	ESTs Weakly similar to HYPOTHETICAL 26.1 KD PROTEIN IN RIB5-SHM1 INTERGENIC REGION (Saccharomyces cerevisiae)	8	TM
RC_AA436370	AA436370	ESTs Highly similar to ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 4 (Rattus norvegicus)	8	other
RC_F01538_s	F01538	RAP1 GTPase activating protein 1	8	other
RC_N39415	N39415	ESTs Highly similar to OSTEOINDUCTIVE FACTOR PRECURSOR (Bos taurus)	8	SS.
RC_W93659	W93659	ESTs	8	other
RC_AA053319	AA053319	ESTs	7.9	TM
RC_AA235009	AA235009	ESTs	7.9	?
RC_AA421750	AA421750	EST	7.9	TM
RC_AA447574	AA447574	ESTs	7.9	other
RC_AA458882	AA458882	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (Homo sapiens)	7.9	?
RC_N33011_s	N33011	Replication protein A (E coli RecA homolog RAD51 homolog)	7.9	other
RC_N53950	N53950	EST - RC_N53950	7.9	other
RC_N69464	N69464	ESTs	7.9	other
RC_R01634	R01634	ESTs	7.9	other
RC_R47948_s	R47948	ESTs	7.9	other
RC_AA150182	AA150182	ESTs Weakly similar to HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III (C.elegans)	7.8	other
RC_AA342084	AA342084	EST - RC_AA342084	7.8	other
RC_AA417213	AA417213	ESTs	7.8	other
RC_AA446486	AA446486	Homo sapiens Ran binding protein 2 (RanBP2alpha) mRNA, partial cds	7.8	?
RC_AA609170	AA609170	EST	7.8	?
RC_N46435	N46435	EST - RC_N46435	7.8	other
RC_N54916	N54916	Human mRNA for KIAA0136 gene, partial cds	7.8	other
RC_AA459389	AA459389	Homo sapiens mRNA for tyrosyl sulfotransferase-2	7.7	TM
RC_AA463693	AA463693	ESTs	7.7	other
RC_T88814	T88814	ESTs	7.7	TM
RC_AA446008	AA446008	EST	7.6	?
RC_H99879	H99879	ESTs Highly similar to EPIDERMAL GROWTH FACTOR PRECURSOR (Mus musculus)	7.6	other
RC_T03306	T03306	Homo sapiens clone 24703 beta-tubulin mRNA, complete cds	7.6	?
RC_T68871	T68871	ESTs	7.6	other
HG2981-HT3938	TIGR - HG2981-HT3938	EST - HG2981-HT3938	7.6	?
U19796	U19796	Human melanoma antigen p15 mRNA, complete cds	7.6	other
AA094752	AA094752	Calcineurin B	7.5	other
RC_AA282074	AA282074	ESTs	7.5	other
RC_AA442767	AA442767	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	7.5	other
RC_AA454566	AA454566	Human mRNA for KIAA0170 gene, complete cds	7.5	?
RC_AA476937_s	AA476937	ESTs	7.5	other
D13666	D13666	Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)	7.5	SS.
RC_N67119	N67119	ESTs	7.5	?
W01296	W01296	EST - W01296	7.5	TM
RC_AA069476_s	AA069476	H.sapiens mRNA for surface glycoprotein	7.4	other
RC_AA287061	AA287061	ESTs	7.4	other
RC_AA410190	AA410190	ESTs	7.4	other
RC_AA411952	AA411952	Homo sapiens mRNA for GalT4 protein	7.4	?
RC_AA412477	AA412477	EST	7.4	?
RC_AA459392	AA459392	ESTs	7.4	other
RC_AA486256	AA486256	ESTs Moderately similar to breast cancer suppressor element Ishmael Upper RP2 (H.sapiens)	7.4	?
RC_AA599042	AA599042	EST	7.4	?
RC_AA609309	AA609309	ESTs	7.4	other

FIGURE 7 (cont.)
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RC_D59489	D59489	ESTs	7.4	SS,TM
RC_N67889	N67889	ESTs	7.4	other
RC_W73520	W73520	ESTs Highly similar to HYPOTHETICAL 28.5 KD PROTEIN ZK1236.7 IN CHROMOSOME III [Caenorhabditis elegans]	7.4	other
X02530	X02530	Interferon (gamma)-induced cell line protein 10 from	7.4	SS.
RC_AA283006	AA283006	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 (Caenorhabditis elegans)	7.3	other
RC_AA426372_s	AA426372	Human mRNA for histone H1x complete cds	7.3	other
RC_AA443794	AA443794	ESTs	7.3	other
RC_AA446869	AA446869	ESTs	7.3	TM
RC_F13642	F13642	ESTs	7.3	other
RC_N21321_i	N21321	ESTs	7.3	?
RC_AA088458	AA088458	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	7.2	other
RC_AA121315	AA121315	ESTs	7.2	other
RC_AA234921	AA234921	ESTs	7.2	other
RC_AA427950	AA427950	EST - RC_AA427950	7.2	?
RC_AA432130	AA432130	ESTs Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	7.2	?
RC_R65593_s	R65593	Homo sapiens mRNA for kynurenine 3-monooxygenase	7.2	TM
RC_AA236177	AA236177	ESTs	7.1	?
RC_AA258482_s	AA258482	Human mRNA for zinc finger protein complete cds	7.1	SS.
RC_AA282143_s	AA282143	H.sapiens mRNA for melanoma growth regulatory protein MIA	7.1	SS.
RC_AA283003	AA283003	ESTs	7.1	other
RC_AA287870_s	AA287870	Lymphotoxin-beta	7.1	other
AA310967_s	AA310967	ESTs Weakly similar to T04A8.11 [C.elegans]	7.1	other
RC_AA410373	AA410373	ESTs	7.1	?
RC_AA421158	AA421158	ESTs	7.1	SS.
C00225_s	C00225	ESTs Highly similar to HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV [Caenorhabditis elegans]	7.1	TM
RC_F13694_f	F13694	ESTs	7.1	?
RC_N29431	N29431	EST - RC_N29431	7.1	?
RC_N67239	N67239	ESTs	7.1	other
RC_T10082_f	T10082	ESTs	7.1	other
RC_AA310499	AA310499	ESTs	7	other
RC_AA449351	AA449351	ESTs Weakly similar to similar to deoxyribose-phosphate aldolase [C.elegans]	7	other
RC_D57389_f	D57389	EST	7	other
RC_N34686	N34686	Homo sapiens clone 23915 mRNA sequence	7	?
RC_Z40345	Z40345	ESTs Weakly similar to T06D8.5 [C.elegans]	7	?
RC_AA410441	AA410441	ESTs	7	TM
RC_AA505093	AA505093	ESTs	6.9	other
RC_N71704	N71704	ESTs	6.9	other
U48705_ma1	U48705	Receptor protein-tyrosine kinase EDDR1	6.9	other
RC_AA127818_i	AA127818	ESTs	6.9	?
RC_AA346385	AA346385	ESTs Highly similar to putative hydrophobic domain in amino acid positions 373-390 [H.sapiens]	6.8	?
RC_AA411204	AA411204	ESTs	6.8	other
RC_AA416876	AA416876	ESTs Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521 [H.sapiens]	6.8	TM
RC_AA419461	AA419461	ESTs	6.8	other
RC_AA446966	AA446966	EST	6.8	other
RC_AA496569	AA496569	ESTs Highly similar to VALYL-TRNA SYNTHETASE [Fugu rubripes]	6.8	other
RC_D51229_f	D51229	Human clone 23589 mRNA sequence	6.8	TM
RC_F02254_s	F02254	H.sapiens mRNA for FAST kinase	6.8	other
RC_H18428_s	H18428	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	6.8	?
RC_AA034069	AA034069	ESTs	6.7	other
RC_AA127058	AA127058	ESTs	6.7	TM
RC_AA435849	AA435849	ESTs Moderately similar to unknown protein [H.sapiens]	6.7	other
RC_H99935_s	H99935	Interleukin 6 signal transducer (gp130 oncostatin M receptor)	6.7	TM
L27841	L27841	Human autoantigen pericentriol material 1 (PCM-1) mRNA complete cds	6.7	other
M11718	M11718	Collagen type V alpha	6.7	?
RC_N50550	N50550	Homo sapiens mRNA for Efs1 complete cds	6.7	other
RC_T92935	T92935	ESTs	6.7	other
U24169	U24169	Human JTV-1 (JTV-1) mRNA complete cds	6.7	other
U30246	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	6.7	TM
RC_AA098834_s	AA098834	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	6.6	TM
RC_AA283198	AA283198	ESTs	6.6	other
RC_AA421782	AA421782	ESTs	6.6	other
RC_AA505141	AA505141	ESTs	6.6	other

FIGURE 7 (cont.)

RC_D60341	D60341	ESTs	6 6	SS.
RC_N26904	N26904	ESTs Highly similar to FK506-BINDING PROTEIN PRECURSOR [Mus musculus]	6 6	TM
RC_R40606	R40606	ESTs Highly similar to SKD3 [M musculus]	6 6	other
RC_R51988	R51988	ESTs	6 6	other
RC_T03790	T03790	ESTs	6 6	other
RC_W72455	W72455	ESTs	6 6	TM
RC_AA100364	AA100364	ESTs	6 5	other
AA236384	AA236384	ESTs Highly similar to COP1 REGULATORY PROTEIN [Arabidopsis thaliana]	6 5	other
RC_AA431085	AA431085	EST	6 5	?
RC_AA446591	AA446591	ESTs	6 5	other
RC_R06700	R06700	ESTs	6.5	other
W49521	W49521	Human prolyl 4-hydroxylase alpha (II) subunit mRNA complete cds	6 5	?
RC_AA195651	AA195651	EST	6 4	?
RC_AA430211	AA430211	ESTs	6 4	other
RC_T15991	T15991	ESTs	6 4	TM
RC_T17119	T17119	ESTs	6 4	TM
U89606	U89606	Human pyridoxal kinase mRNA complete cds	6 4	other
X54326	X54326	MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE	6.4	other
RC_AA157814	AA157814	ESTs	6.3	other
RC_AA443658	AA443658	Homo sapiens lamin B receptor homolog TM7SF2 (TM7SF2) mRNA complete cds	6 3	TM
RC_AA621169	AA621169	ESTs	6.3	other
RC_D20168	D20168	Human mRNA for KIAA0050 gene complete cds	6.3	other
D81608	D81608	H.sapiens mRNA for RNA polymerase II subunit	6.3	TM
RC_H57330	H57330	EST	6 3	?
L77701	L77701	Homo sapiens COX17 mRNA complete cds	6 3	other
RC_N48166	N48166	ESTs	6 3	other
RC_R65826	R65826	Homo sapiens mRNA for KIAA0549 protein partial cds	6 3	SS.
W19662	W19662	ESTs	6.3	other
X70649	X70649	Homo sapiens DDX1 gene complete CDS	6 2	?
RC_AA024664_s	AA024664	Human NADH.ubiquinone oxidoreductase subunit B13 (B13) mRNA complete cds	6 2	other
RC_AA098874	AA098874	ESTs	6 2	other
RC_AA152178	AA152178	ESTs	6 2	other
RC_AA279943	AA279943	ESTs	6 2	other
RC_AA412106	AA412106	ESTs	6 2	other
RC_AA621721	AA621721	ESTs	6 2	other
RC_N38959_f	N38959	Homo sapiens chaperonin containing t-complex polypeptide 1 beta subunit (Cctb) mRNA complete cds	6.2	TM
U40271	U40271	Protein-tyrosine kinase 7	6 2	?
X52150_rna1_s	X52150	Arylsulfatase A	6 2	other
X86018	X86018	H sapiens mRNA for MUF1 protein	6 1	?
RC_AA133199	AA133199	ESTs	6 1	other
RC_AA398740	AA398740	ESTs	6 1	other
RC_AA405505	AA405505	Homo sapiens mRNA for putative RNA helicase 3' end	6 1	other
RC_AA416568	AA416568	ESTs	6 1	?
RC_AA448349	AA448349	ESTs	6 1	TM
AA455331	AA455331	ESTs	6 1	other
RC_AA479933_f	AA479933	ESTs	6 1	other
RC_AA521080	AA521080	ESTs	6 1	TM
RC_AA600257_s	AA600257	ERGIC-53 PROTEIN PRECURSOR	6 1	other
RC_D20280	D20280	ESTs	6 1	other
RC_H55748	H55748	ESTs	6 1	?
RC_H55915	H55915	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H sapiens]	6.1	other
L32137	L32137	Human germline oligomeric matrix protein (COMP) mRNA complete cds	6 1	?
L37747_s	L37747	LAMIN B1	6 1	SS.
RC_N92593	N92593	ESTs	6 1	?
RC_R99978	R99978	ESTs Weakly similar to line-1 protein ORF2 [H sapiens]	6 1	?
RC_T77733_s	T77733	Tubulin gamma polypeptide	6 1	other
U78525	U78525	Human eukaryotic translation initiation factor (eIF3) mRNA complete cds	6 1	other
RC_W69807	W69807	ESTs Highly similar to GOLIATH PROTEIN [Drosophila melanogaster]	6	?
RC_AA406137	AA406137	EST	6	other
RC_AA521103	AA521103	ESTs	6	other
RC_AA609277	AA609277	ESTs	6	other
J04177	J04177	Collagen type XI alpha 1	6	?
RC_R33663_s	R33663	ESTs		

FIGURE 7 (cont.)
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			6	other
RC_T16660	T16660	ESTs	6	other
U73514	U73514	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase (SCHAD) mRNA complete cds	5.9	other
RC_AA223730	AA223730	ESTs	5.9	other
RC_AA292655	AA292655	ESTs	5.9	other
RC_N26391	N26391	ESTs	5.9	other
RC_N50744	N50744	ESTs	5.9	TM
RC_T88953	T88953	ESTs	5.9	?
HG3748-HT4018	TIGR - HG3748-HT4018	EST - HG3748-HT4018	5.9	other
RC_W38407	W38407	ESTs	5.9	?
RC_W63563_s	W63563	Homo sapiens scaffold attachment factor B (SAF-B) mRNA partial cds	5.9	other
RC_Z41619_s	Z41619	ESTs Weakly similar to keratin 8 type II cytoskeletal embryonic [M musculus]	5.8	other
RC_AA279292	AA279292	ESTs	5.8	other
RC_AA287665	AA287665	ESTs	5.8	TM
RC_AA422007	AA422007	ESTs	5.8	TM
RC_AA425379	AA425379	ESTs	5.8	?
RC_AA427925_s	AA427925	ESTs Weakly similar to PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [Homo sapiens]	5.8	other
RC_AA430673	AA430673	ESTs	5.8	other
RC_AA441801	AA441801	ESTs	5.8	other
RC_AA463740_s	AA463740	ESTs	5.8	TM
RC_H89987_s	H89987	Human multidrug resistance-associated protein homolog (MRP5) mRNA partial cds	5.8	other
RC_H94843	H94843	ESTs	5.8	other
M25753	M25753	Cyclin B1	5.8	other
RC_N80183	N80183	ESTs	5.8	other
RC_T67463_s	T67463	CATHEPSIN K PRECURSOR	5.8	?
U65932	U65932	Human extracellular matrix protein 1 (ECM1) mRNA complete cds	5.7	TM
RC_AA149624	AA149624	Homo sapiens mRNA for follistatin-related protein (FRP) complete cds	5.7	other
RC_AA192334	AA192334	ESTs	5.7	?
RC_AA207105	AA207105	EST	5.7	other
RC_AA442763	AA442763	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]	5.7	other
AA443251	AA443251	ESTs	5.7	other
RC_AA454562	AA454562	ESTs	5.7	other
RC_AA459945	AA459945	Homo sapiens mRNA for KIAA0585 protein partial cds	5.7	other
RC_AA478794	AA478794	ESTs	5.7	other
RC_AA609473	AA609473	ESTs	5.7	other
RC_F09058	F09058	ESTs	5.7	other
RC_H54430	H54430	ESTs	5.7	?
M34677	M34677	FACTOR VIII INTRON 22 PROTEIN	5.7	other
RC_N27563	N27563	ESTs	5.7	other
RC_R02572	R02572	Fibronectin 1	5.7	?
RC_R09166	R09166	ESTs	5.7	other
RC_R85829	R85829	EST	5.7	?
HG2981-HT3125	TIGR - HG2981-HT3125	EST - HG2981-HT3125	5.7	other
U56402	U56402	Homo sapiens clone 24522 mRNA sequence	5.7	other
W30943	W30943	ESTs	5.6	other
RC_AA040154	AA040154	ESTs	5.6	other
AA116095	AA116095	ESTs Weakly similar to T12D8.1 [C.elegans]	5.6	TM
RC_AA147884	AA147884	ESTs	5.6	?
RC_AA149754_i	AA149754	EST	5.6	other
RC_AA232956	AA232956	ESTs	5.6	other
RC_AA397919	AA397919	ESTs	5.6	other
RC_AA398212	AA398212	ESTs	5.6	other
RC_AA398264	AA398264	Homo sapiens clone 23736 mRNA sequence	5.6	other
RC_AA406169	AA406169	Homo sapiens KIAA0431 mRNA partial cds	5.6	TM
RC_AA416986	AA416986	Guanine nucleotide binding protein (G protein) beta polypeptide 1	5.6	TM
RC_AA435742_s	AA435742	Human fatty acid amide hydrolase mRNA complete cds	5.6	?
RC_AA435936	AA435936	EST	5.6	other
RC_AA436819	AA436819	ESTs	5.6	other
RC_AA452842	AA452842	ESTs	5.6	other
RC_AA453987	AA453987	ESTs	5.6	other
AA477214	AA477214	ESTs	5.6	TM
RC_AA482269	AA482269	Integral transmembrane protein 1	5.6	TM
D50914	D50914	Human mRNA for KIAA0124 gene partial cds		

FIGURE 7 (cont.)

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RC_N51590_s	N51590	ESTs	5.6	other
RC_N93797	N93797	ESTs	5.6	SS.
RC_T23528	T23528	ESTs Moderately similar to TYKi protein [M.musculus]	5.6	other
RC_T95057_f	T95057	ESTs	5.6	other
U91327	U91327	EST - U91327	5.6	?
X76105	X76105	H.sapiens DAP-1 mRNA	5.6	other
RC_AA021182	AA021182	ESTs	5.5	other
RC_AA075200	AA075200	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8	5.5	other
RC_AA085589	AA085589	ESTs Highly similar to TRANSLATION INITIATION FACTOR EIF-2B-DELTA SUBUNIT [Oryctolagus cuniculus]	5.5	other
RC_AA115535	AA115535	ESTs	5.5	other
RC_AA195517	AA195517	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	5.5	TM
RC_AA280840	AA280840	ESTs	5.5	SS.
RC_AA443602	AA443602	ESTs	5.5	TM
RC_AA609996	AA609996	ESTs Highly similar to Surf-4 protein [M.musculus]	5.5	?
RC_H99500	H99500	Homo sapiens mRNA for follistatin-related protein (FRP) complete cds	5.5	other
M24486	M24486	Procollagen-proline 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase) alpha polypeptide	5.5	SS.
RC_N21032	N21032	EST	5.5	?
RC_N22015	N22015	ESTs	5.5	TM
RC_R43883	R43883	ESTs	5.5	other
U09278	U09278	Human fibroblast activation protein mRNA complete cds	5.5	SS.
X02874	X02874	(2'-5') oligoadenylate synthetase E	5.5	other
RC_AA242757	AA242757	ESTs	5.4	other
RC_AA251973	AA251973	ESTs	5.4	?
RC_AA293773	AA293773	Homo sapiens clone 23870 mRNA sequence	5.4	other
RC_AA398721	AA398721	EST - RC_AA398721	5.4	other
RC_AA437225	AA437225	ESTs	5.4	other
RC_AA448410	AA448410	ESTs	5.4	other
RC_AA449357	AA449357	ESTs	5.4	other
RC_AA479348_s	AA479348	H.sapiens mRNA for SYT	5.4	other
C02170	C02170	ESTs Weakly similar to weak similarity to ribosomal protein L14 [C elegans]	5.4	other
RC_H75933_f	H75933	Laminin receptor (2H5 epitope)	5.4	other
M97936	M97936	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	5.4	other
RC_N51917	N51917	ESTs	5.4	other
RC_R41294_s	R41294	ESTs	5.4	?
RC_T81310	T81310	EST	5.4	TM
RC_W45275_f	W45275	CD44 antigen (cell adhesion molecule)	5.4	other
RC_W92001	W92001	ESTs	5.3	other
RC_AA135809	AA135809	ESTs	5.3	TM
RC_AA157811	AA157811	EST - RC_AA157811	5.3	other
RC_AA191524	AA191524	ESTs	5.3	?
RC_AA195036_s	AA195036	Human Ro/SSA ribonucleoprotein homolog (RoRet) mRNA complete cds	5.3	other
RC_AA284565_f	AA284565	ESTs	5.3	other
RC_AA287022_s	AA287022	Thymidine kinase 1 soluble	5.3	other
RC_AA394071	AA394071	Homo sapiens gamma2-adaptin (G2AD) mRNA complete cds	5.3	?
RC_AA399477	AA399477	ESTs	5.3	TM
RC_AA401428_s	AA401428	NUCLEAR PORE COMPLEX PROTEIN NUP214	5.3	other
RC_AA425154	AA425154	ESTs	5.3	other
RC_AA447213_s	AA447213	ESTs Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]	5.3	other
RC_AA464860	AA464860	Homo sapiens Jak2 kinase mRNA complete cds	5.3	other
RC_AA465191	AA465191	ESTs	5.3	TM
RC_AA476293	AA476293	ESTs Weakly similar to DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT [Plasmodium falciparum]	5.3	other
RC_H80749	H80749	ESTs	5.3	other
RC_N94385_s	N94385	Human germline oligomeric matrix protein (COMP) mRNA complete cds	5.3	other
U59877	U59877	Human low-Mr GTP-binding protein (RAB31) mRNA complete cds	5.3	TM
X03363	X03363	ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR	5.2	other
RC_AA005262	AA005262	Homo sapiens DNA sequence from PAC 262D12 on chromosome q23.3-24.3 Contains a Tenascin (Hexabrachion Cytotactin Neuronectin Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosom	5.2	?
RC_AA025370	AA025370	ESTs	5.2	other
RC_AA026682_s	AA026682	Topoisomerase (DNA) II alpha (170kD)	5.2	?
RC_AA279160	AA279160	ESTs	5.2	other
RC_AA403116	AA403116	Homo sapiens U-snRNP-associated cyclophilin (USA-CyP) mRNA complete cds	5.2	?
RC_AA452857	AA452857	ESTs	5.2	other
RC_AA488280	AA488280	EST - RC_AA488280		

FIGURE 7 (cont.)

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RC_AA599140	AA599140	ESTs Moderately similar to ZINC FINGER PROTEIN 7 [Homo sapiens]	5.2	other
RC_AA609891	AA609891	EST	5.2	?
RC_AA621714	AA621714	ESTs	5.2	other
H87319	H87319	Protein kinase C substrate 80K-H	5.2	TM
RC_H96392	H96392	ESTs	5.2	other
RC_N54321	N54321	EST	5.2	?
RC_N73861	N73861	EST - RC_N73861	5.2	other
RC_R05312_s	R05312	ESTs	5.2	other
RC_R59183_f	R59183	ESTs	5.2	other
RC_R92205	R92205	ESTs	5.2	TM
RC_W45302	W45302	ESTs Highly similar to HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III [Caenorhabditis elegans]	5.2	other
X17644	X17644	G1 to S phase transition 1	5.2	other
RC_AA284518	AA284518	ESTs	5.1	other
RC_AA434152	AA434152	ESTs	5.1	SS,
RC_AA436673	AA436673	ESTs	5.1	other
RC_AA481453	AA481453	ESTs	5.1	other
RC_AA487449	AA487449	EST - RC_AA487449	5.1	other
RC_AA491465	AA491465	ESTs	5.1	other
RC_N79612	N79612	ESTs	5.1	other
RC_N98461	N98461	ESTs	5.1	TM
RC_R42036	R42036	ESTs	5.1	other
RC_R43543	R43543	ESTs	5.1	other
RC_W59961_s	W59961	Human mRNA for KIAA0389 gene complete cds	5.1	other
RC_W60180	W60180	ESTs	5.1	other
Y09912_mat	Y09912	H.sapiens mRNA for AP-2 beta transcription factor	5.1	?
RC_AA055892	AA055892	ESTs	5	other
RC_AA085676	AA085676	ESTs Weakly similar to TYL [H.sapiens]	5	other
RC_AA172056	AA172056	ESTs	5	other
RC_AA211400	AA211400	ESTs	5	other
RC_AA236356	AA236356	ESTs	5	other
RC_AA252395	AA252395	ESTs	5	?
RC_AA262179	AA262179	ESTs	5	other
RC_AA281451	AA281451	ESTs	5	other
RC_AA287095	AA287095	EST - RC_AA287095	5	?
RC_AA425691	AA425691	ESTs	5	other
RC_AA426376	AA426376	ESTs	5	other
RC_AA446000	AA446000	ESTs	5	other
RC_AA478951	AA478951	EST	5	?
AA479995	AA479995	Homo sapiens mRNA for KIAA0583 protein partial cds	5	other
D82419	D82419	ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD [Saccharomyces cerevisiae]	5	TM
RC_F02080_f	F02080	ESTs	5	other
RC_F10496_f	F10496	H.sapiens 40 kDa protein kinase related to rat ERK2	5	other
J00314	J00314	Homo sapiens clone 24703 beta-tubulin mRNA complete cds	5	?
J05614	J05614	EST - J05614	5	?
M16336	M16336	CD2 antigen (T cell surface antigen T11)	5	TM
M80244	M80244	INTEGRAL MEMBRANE PROTEIN E16	5	TM
RC_N33927_s	N33927	"Homo sapiens mRNA for histone H2B clone pJG4-5-15""	5	SS,
RC_N73808_f	N73808	ESTs	5	?
RC_T79815	T79815	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	5	other
U62392	U62392	Homo sapiens zinc finger protein mRNA complete cds	5	other
RC_AA133756	AA133756	ESTs	4.9	other
RC_AA234559	AA234559	ESTs	4.9	other
RC_AA490830	AA490830	ESTs	4.9	other
C01169	C01169	Homo sapiens clone 23915 mRNA sequence	4.9	other
D21255	D21255	Cadherin 11 (OB-cadherin)	4.9	SS,TM
RC_F10945	F10945	Polypyrimidine tract binding protein (hnRNP I) (alternative products)	4.9	other
RC_H24044	H24044	Protein phosphatase 2 (formerly 2A) catalytic subunit alpha isoform	4.9	other
RC_N34893	N34893	ESTs Highly similar to HYPOTHETICAL 47.8 KD PROTEIN B0280.9 IN CHROMOSOME III [Caenorhabditis elegans]	4.9	other
RC_R41772	R41772	EST	4.9	?
RC_T59338	T59338	EST - RC_T59338	4.9	other
RC_AA191512	AA191512	ESTs	4.8	?
RC_AA400513_f	AA400513	ESTs	4.8	other
RC_AA406081	AA406081	ESTs	4.8	other

FIGURE 7 (cont.)

RC_AA448158	AA448158	EST	4.8	?
RC_N94362	N94362	EST	4.8	?
RC_W60007_s	W60007	Human mRNA for KIAA0203 gene complete cds	4.8	other
RC_AA026356	AA026356	ESTs	4.7	?
AA075599	AA075599	ESTs Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT [Bos taurus]	4.7	other
RC_AA157836	AA157836	ESTs	4.7	other
RC_AA196549	AA196549	ESTs	4.7	other
RC_AA404352	AA404352	ESTs	4.7	SS.
RC_AA417321	AA417321	ESTs Weakly similar to CALMODULIN [D.melanogaster]	4.7	other
RC_AA418074	AA418074	ESTs	4.7	other
RC_N32919	N32919	ESTs	4.6	?
RC_AA177051	AA177051	EST - RC_AA177051	4.6	TM
RC_AA453483	AA453483	ESTs	4.6	SS.TM
RC_AA620795	AA620795	ESTs	4.6	other
RC_H97012	H97012	ESTs Weakly similar to L8004.7 gene product [S.cerevisiae]	4.6	other
M34458_ma1	M34458	LAMIN B1	4.6	other
RC_N68921	N68921	ESTs	4.6	other
U18321	U18321	H.sapiens DAP-3 mRNA	4.6	?
X17059	X17059	ARYLAMINE N-ACETYLTRANSFERASE MONOMORPHIC	4.5	?
RC_AA210722	AA210722	EST	4.5	other
RC_AA255605	AA255605	Homo sapiens spindle pole body protein spc97 homolog GCP2 mRNA complete cds	4.5	?
RC_AA443634	AA443634	Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA complete cds	4.5	TM
RC_AA461507	AA461507	ESTs	4.5	other
RC_AA464853	AA464853	ESTs Weakly similar to T01G9.4 [C.elegans]	4.5	?
RC_N71076	N71076	EST	4.5	other
RC_T40841	T40841	ESTs	4.5	other
X57766	X57766	Human stromelysin-3 mRNA	4.4	other
RC_AA206497_s	AA206497	PROTEASOME COMPONENT C9	4.4	other
RC_AA227900_s	AA227900	H.sapiens mRNA homologous to S. cerevisiae RAD54	4.4	?
RC_AA346495	AA346495	ESTs Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	4.4	?
RC_AA386260	AA386260	EST	4.4	other
RC_AA398155	AA398155	ESTs	4.4	SS.
RC_AA405569_s	AA405569	Human fibroblast activation protein mRNA complete cds	4.4	other
AA422025_s	AA422025	ESTs	4.4	other
RC_AA430124	AA430124	ESTs	4.4	other
RC_AA453466	AA453466	ESTs	4.4	other
RC_AA463726_s	AA463726	Homo sapiens mRNA for JM27 protein complete CDS (clone IMAGE 145745 and IMAGE 257878)	4.4	other
RC_C20981	C20981	ESTs Highly similar to CHOLINE DEHYDROGENASE [Escherichia coli]	4.4	?
RC_R70801_s	R70801	EST	4.4	TM
RC_T97307	T97307	EST - RC_T97307	4.4	?
U28386	U28386	RAG (recombination activating gene) cohort 1	4.3	other
X02419_ma1	X02419	Urokinase-type plasminogen activator	4.3	TM
RC_AA235112	AA235112	ESTs	4.3	SS.
RC_AA453176_s	AA453176	Human protein kinase ATR mRNA complete cds	4.3	other
D42073	D42073	Human mRNA for reticulocalbin complete cds	4.3	?
U21090	U21090	Human DNA polymerase delta small subunit mRNA complete cds	4.3	other
U24389	U24389	Human lysyl oxidase-like protein mRNA complete cds	4.2	other
U73379	U73379	Human cyclin-selective ubiquitin carrier protein mRNA complete cds	4.2	other
RC_AA227959_s	AA227959	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA complete cds	4.2	SS.
RC_AA416931	AA416931	ESTs	4.2	other
RC_AA419200	AA419200	ESTs	4.2	TM
RC_H18947	H18947	ESTs	4.2	SS.
RC_H25577	H25577	ESTs Highly similar to CYTOCHROME P450 IVB1 [Oryctolagus cuniculus]	4.2	?
RC_H90161_s	H90161	ESTs	4.2	other
M15796	M15796	Proliferating cell nuclear antigen	4.2	other
RC_R46482	R46482	ESTs	4.2	TM
S74445	S74445	Cellular retinoic acid-binding protein [human skin mRNA 735 nt]	4.2	other
U74612	U74612	Human putative M phase phosphoprotein 2 (MPP2) mRNA complete cds	4.1	other
X62534	X62534	High-mobility group (nonhistone chromosomal) protein 2	4.1	other
RC_AA398369	AA398369	ESTs	4.1	TM
RC_AA448347	AA448347	Annexin XI (56kD autoantigen)	4.1	TM
RC_AA464707	AA464707	ESTs		
RC_AA478799_s	AA478799	H.sapiens mRNA for BS69 protein		

FIGURE 7 (cont.)

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RC_AA496369	AA496369	ESTs	4.1	other
RC_D54296_f	D54296	Human mRNA for KIAA0255 gene complete cds	4.1	TM
RC_N66818	N66818	ESTs	4.1	TM
U50648	U50648	Protein kinase interferon-inducible double stranded RNA dependent	4.1	?
AA193297	AA193297	ESTs	4	SS
RC_AA228026	AA228026	ESTs Highly similar to PBDX protein [H.sapiens]	4	TM
RC_AA287325_f	AA287325	ESTs	4	?
RC_AA287596	AA287596	ESTs	4	other
RC_AA421041	AA421041	ESTs	4	other
U29463	U29463	Cytochrome B561	4	?
RC_W87752_s	W87752	Small inducible cytokine A5 (RANTES)	4	TM
X94563_xpt2_r	X94563	EST - X94563_xpt2_r	4	?
RC_AA256837_i	AA256837	ESTs	3.9	?
RC_AA416627_s	AA416627	ESTs	3.9	other
RC_AA482224_f	AA482224	ESTs Weakly similar to No definition line found [C.elegans]	3.9	?
RC_AA485360	AA485360	EST	3.9	?
RC_R44709	R44709	Homo sapiens mRNA for RB18A protein	3.9	other
RC_W45572_f	W45572	ADP-ribosylation factor 1	3.9	other
RC_AA132366	AA132366	Homo sapiens mRNA for SPOP	3.8	?
RC_AA133527	AA133527	ESTs Moderately similar to The KIAA0138 gene product is novel. [H sapiens]	3.8	other
RC_AA224324	AA224324	ESTs	3.8	other
RC_AA287642_s	AA287642	Human mRNA for KIAA0078 gene complete cds	3.8	other
RC_AA425652	AA425652	ESTs	3.8	other
RC_AA459960_s	AA459960	ESTs Weakly similar to D9481.16 gene product [S.cerevisiae]	3.8	other
RC_AA465094	AA465094	ESTs Weakly similar to nemo form II [D.melanogaster]	3.8	other
RC_AA485451	AA485451	EST	3.8	other
RC_AA599244	AA599244	Homo sapiens mRNA for KIAA0530 protein partial cds	3.8	other
RC_N41018	N41018	Human mRNA for prepro cortistatin like peptide complete cds	3.8	?
RC_N74501	N74501	ESTs	3.8	other
RC_N98525	N98525	Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA complete cds	3.8	other
W46488	W46488	Homo sapiens Amplified in Breast Cancer (AIB1) mRNA complete cds	3.8	other
RC_AA232183	AA232183	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H sapiens]	3.7	other
RC_AA399547	AA399547	ESTs	3.7	other
RC_AA424486	AA424486	ESTs	3.7	TM
RC_AA598661	AA598661	ESTs	3.7	other
RC_H04339	H04339	ESTs	3.7	TM
M14219	M14219	Decorin	3.7	other
M25077	M25077	Human 60-kdal ribonucleoprotein (Ro) mRNA complete cds	3.7	?
RC_N67102_s	N67102	ESTs	3.7	other
RC_W45728	W45728	ESTs Highly similar to HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN L [Homo sapiens]	3.7	other
Y12394	Y12394	Homo sapiens importin-alpha homolog (SRP1gamma) mRNA complete cds	3.7	other
RC_AA401758_i	AA401758	ESTs Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	3.6	SS
RC_AA435840	AA435840	Homo sapiens mRNA for high mobility group protein HMG2a	3.6	other
RC_AA461492	AA461492	ESTs	3.6	other
RC_AA521240	AA521240	ESTs	3.6	TM
RC_F02450	F02450	ESTs Moderately similar to unknown protein [H.sapiens]	3.6	TM
RC_N63823	N63823	ESTs	3.6	other
RC_N67603	N67603	ESTs Weakly similar to hypothetical L1 protein [H sapiens]	3.6	?
RC_N91887_s	N91887	Homo sapiens mRNA for NB thymosin beta complete cds	3.6	other
RC_N93967	N93967	EST	3.6	other
RC_W73788	W73788	ESTs	3.6	other
RC_AA034365	AA034365	NUCLEAR PORE GLYCOPROTEIN P62	3.5	other
RC_AA083069	AA083069	EST - RC_AA083069	3.5	?
RC_AA112063	AA112063	ESTs Weakly similar to PRE-MRNA SPLICING HELICASE BRR2 [S.cerevisiae]	3.5	other
RC_AA126951	AA126951	ESTs Weakly similar to DNA-directed RNA polymerase [D.melanogaster]	3.5	other
RC_AA159181	AA159181	ESTs Weakly similar to Lpa8p [S cerevisiae]	3.5	other
RC_AA398450	AA398450	H sapiens mRNA for synaptonemal complex lateral element protein	3.5	other
RC_AA404593	AA404593	ESTs	3.5	other
RC_AA412739	AA412739	EST	3.5	other
RC_AA447626	AA447626	EST	3.5	?
RC_AA453787_s	AA453787	Human TFIIB related factor hBRF (HBRF) mRNA complete cds	3.5	other
RC_AA599106	AA599106	EST - RC_AA599106	3.5	other
D82558	D82558	Homo sapiens KB07 protein mRNA partial cds	3.5	other

FIGURE 7 (cont.)

RC_H72283_s	H72283	Human mRNA for KIAA0265 gene partial cds	3.5	other
L38961	L38961	Integral transmembrane protein 1	3.5	TM
RC_N36835	N36835	ESTs	3.5	other
RC_N90859	N90859	ESTs	3.5	other
RC_R63734	R63734	ESTs	3.5	TM
R70167	R70167	ESTs	3.5	other
X69141	X69141	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE	3.5	other
X75346	X75346	H.sapiens mRNA for MAP kinase activated protein kinase	3.5	TM
RC_AA029042	AA029042	Human hSIAH2 mRNA complete cds	3.4	other
RC_AA100470	AA100470	ESTs	3.4	other
AA115397	AA115397	Homo sapiens mRNA for putative methyltransferase	3.4	other
RC_AA164209	AA164209	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds	3.4	other
RC_AA258203	AA258203	ESTs	3.4	other
RC_AA411448_s	AA411448	ESTs	3.4	TM
RC_AA429917	AA429917	ESTs	3.4	TM
RC_AA442070_s	AA442070	Phosphoribosyl pyrophosphate amidotransferase	3.4	other
RC_AA449417	AA449417	Homo sapiens mRNA for putative glucosyltransferase partial cds	3.4	TM
RC_AA453164	AA453164	EST	3.4	?
RC_F10326_f	F10326	EST	3.4	other
RC_H88639	H88639	ESTs	3.4	other
L47276	L47276	EST - L47276	3.4	other
RC_N29740	N29740	ESTs	3.4	other
RC_N33920	N33920	H.sapiens mRNA for diubiquitin	3.4	other
RC_N34895	N34895	ESTs	3.4	other
S81003	S81003	L-UBC	3.4	other
U07806	U07806	DNA topoisomerase I	3.4	other
RC_AA047896	AA047896	ESTs	3.3	other
RC_AA116036	AA116036	ESTs	3.3	other
RC_AA232535_s	AA232535	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]	3.3	other
RC_AA435847	AA435847	EST - RC_AA435847	3.3	other
RC_AA453159_s	AA453159	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds	3.3	other
RC_AA490899	AA490899	ESTs	3.3	other
RC_AA496051	AA496051	ESTs	3.3	TM
AD000092_cds7	AD000092	Homo sapiens DNA from chromosome 19p13.2 cosmids R31240 R30272 and R28549 containing the EKLF GCDH CRTC and RAD23A genes genomic sequence	3.3	?
RC_F09353	F09353	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene complete cds	3.3	other
RC_N34059	N34059	EST - RC_N34059	3.3	other
RC_N58172	N58172	ESTs Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]	3.3	TM
RC_N67437	N67437	ESTs	3.3	TM
RC_R24237_f	R24237	ESTs	3.3	?
RC_R45356	R45356	Homo sapiens cDNA similar to RNA binding protein C elegans complete	3.3	other
RC_W44735	W44735	ESTs	3.3	?
RC_W85861	W85861	ESTs Weakly similar to ZK1058 4 [C elegans]	3.3	SS.TM
RC_AA134965_r	AA134965	ESTs	3.2	other
RC_AA169379	AA169379	ESTs	3.2	other
RC_AA211941	AA211941	Homo sapiens polyadenylate binding protein-interacting protein-1 (PAIP1) mRNA complete cds	3.2	other
RC_AA232939	AA232939	ESTs	3.2	other
AA421213	AA421213	ESTs Weakly similar to F28F8 3 [C.elegans]	3.2	other
RC_AA422079	AA422079	ESTs Weakly similar to RAR-RESPONSIVE PROTEIN TIG1 [H sapiens]	3.2	other
RC_AA448213_s	AA448213	Human myogenic repressor I-mf (MDFI) mRNA complete cds	3.2	TM
RC_AA490969	AA490969	ESTs	3.2	other
RC_AA609423	AA609423	ESTs	3.2	other
D84145	D84145	Human WS-3 mRNA complete cds	3.2	other
RC_F09315	F09315	Homo sapiens mRNA for KIAA0583 protein partial cds	3.2	other
L07515	L07515	HETEROCHROMATIN PROTEIN 1 HOMOLOG	3.2	other
M86852	M86852	Peroxisomal membrane protein 3 (35kD Zellweger syndrome)	3.2	TM
RC_N35385	N35385	ESTs	3.2	other
RC_N78572	N78572	EST - RC_N78572	3.2	other
RC_R60192_s	R60192	Peroxisomal biogenesis factor 7	3.2	other
RC_R67996	R67996	ESTs	3.2	other
RC_T15665	T15665	ESTs Weakly similar to HYPOTHETICAL 139 1 KD PROTEIN C08B11 3 IN CHROMOSOME II [C elegans]	3.2	other
T40327_s	T40327	ESTs	3.2	other
RC_T65797	T65797	ESTs Weakly similar to Pin1 protein [H sapiens]	3.2	TM

FIGURE 7 (cont.)

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U37547	U37547	Human IAP homolog B (MIHB) mRNA complete cds	3.2	other
U51586	U51586	Human siah binding protein 1 (SiahBP1) mRNA partial cds	3.2	other
U81554	U81554	Homo sapiens signal recognition particle 72 (SRP72) mRNA complete cds	3.2	other
RC_W33134_s	W33134	ESTs	3.2	?
RC_W46255	W46255	ESTs	3.2	other
Z97054_xpt2	Z97054	Human mRNA for KIAA0312 gene partial cds	3.2	?
RC_AA047036	AA047036	ESTs	3.1	other
RC_AA150043	AA150043	ESTs	3 1	TM
RC_AA232874	AA232874	EST	3 1	TM
RC_AA291259	AA291259	ESTs	3.1	TM
RC_AA398360	AA398360	EST	3.1	?
RC_AA401687_s	AA401687	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds	3 1	other
RC_D60208_f	D60208	ESTs	3 1	other
D87466	D87466	Human mRNA for KIAA0276 gene partial cds	3.1	other
RC_N21626	N21626	ESTs	3.1	other
RC_N69331	N69331	Peptidylprolyl isomerase C (cyclophilin C)	3.1	TM
S66431	S66431	Homo sapiens clone 23592 mRNA sequence	3.1	other
RC_W44928	W44928	ESTs	3 1	TM
RC_W72967	W72967	ESTs	3.1	other
X17620	X17620	NUCLEOSIDE DIPHOSPHATE KINASE A	3.1	other
X59798	X59798	Cyclin D1 (PRAD1 parathyroid adenomatosis 1)	3.1	other
RC_AA099719	AA099719	ESTs	3	other
RC_AA152305_s	AA152305	Interferon (gamma)-induced cell line protein 10 from	3	SS.
RC_AA227932	AA227932	ESTs	3	other
RC_AA251738	AA251738	H sapiens mRNA for TAFII100 protein	3	other
RC_AA386264	AA386264	ESTs Highly similar to ribosome-binding protein p34 [R.norvegicus]	3	other
RC_AA406577	AA406577	ESTs	3	other
RC_AA423827_r	AA423827	ESTs	3	other
RC_N47204	N47204	ESTs Weakly similar to C50F4.12 [C.elegans]	3	other
RC_R36548	R36548	ESTs	3	TM
S50223	S50223	HKR-T1	3	other
RC_W46286_s	W46286	ESTs Weakly similar to ZK1058.5 [C.elegans]	3	TM
RC_W80482	W80482	ESTs	3	other
X70944_s	X70944	PTB-ASSOCIATED SPLICING FACTOR	3	other
X74801	X74801	H sapiens Cctg mRNA for chaperonin	3	other
Y12065	Y12065	Homo sapiens mRNA for nucleolar protein hNop56	3	?
RC_AA164293_f	AA164293	ESTs	2.9	?
RC_AA179845	AA179845	ESTs Moderately similar to rabkinesin-6 [M musculus]	2.9	other
RC_AA195936	AA195936	ESTs Weakly similar to W02D9.2 [C.elegans]	2.9	TM
AA203523	AA203523	ESTs Weakly similar to coded for by C. elegans cDNA yk10c10 3 [C elegans]	2.9	other
RC_AA206088	AA206088	ESTs	2 9	other
RC_AA213506	AA213506	ESTs	2.9	other
RC_AA228020	AA228020	Homo sapiens splicing factor (CC1.3) mRNA complete cds	2.9	other
RC_AA242834	AA242834	ESTs	2 9	other
RC_AA279420	AA279420	ESTs Weakly similar to T08A11.2 [C.elegans]	2 9	TM
RC_AA292747	AA292747	ESTs	2 9	other
AA393164_s	AA393164	Homo sapiens mammaglobin B precursor mRNA complete cds	2.9	TM
RC_AA399164	AA399164	ESTs	2.9	other
RC_AA399264	AA399264	ESTs	2 9	other
RC_AA400725	AA400725	ESTs	2 9	other
RC_AA426120	AA426120	EST - RC_AA426120	2.9	other
AA452011	AA452011	ESTs Highly similar to deduced protein product shows significant homology to coactosin from Dictyostelium discoideum [H sapiens]	2.9	other
RC_AA485214_s	AA485214	DNA-BINDING PROTEIN NEFA PRECURSOR	2.9	SS.
D00596	D00596	Thymidylate synthase	2.9	?
RC_D60061_s	D60061	ESTs	2.9	other
RC_F13779	F13779	ESTs	2.9	SS.
RC_H16790	H16790	ESTs	2.9	other
RC_H97677_s	H97677	ESTs	2 9	other
M28211	M28211	Homo sapiens GTP-binding protein (RAB4) mRNA complete cds	2.9	other
RC_N32333	N32333	Homo sapiens M962 protein spliced isoform 2 mRNA complete cds	2 9	other
RC_N36881	N36881	ESTs	2 9	other
RC_R50840	R50840	H sapiens mRNA for ras-related GTP-binding protein	2.9	other
RC_R97040	R97040	ESTs	2 9	other

FIGURE 7 (cont.)
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RC_T25732_f	T25732	Human mRNA for KIAA0252 gene partial cds	2.9	?
T54762_s	T54762	ESTs	2.9	?
HG110-HT110	TIGR - HG110-HT110	EST - HG110-HT110	2.9	?
U40714	U40714	Human tyrosyl-tRNA synthetase mRNA complete cds	2.9	other
RC_AA001409_r	AA001409	ESTs	2.8	other
RC_AA128407	AA128407	ESTs	2.8	other
RC_AA232231	AA232231	ESTs	2.8	other
RC_AA262768	AA262768	ESTs	2.8	TM
RC_AA292765	AA292765	H.sapiens mRNA for M-phase phosphoprotein mpp5	2.8	other
RC_AA310729_s	AA310729	Human mRNA for clathrin-like protein complete cds	2.8	TM
RC_AA405512	AA405512	ESTs	2.8	other
RC_AA411532	AA411532	ESTs Weakly similar to ORF YOR285w [S.cerevisiae]	2.8	other
RC_AA412497	AA412497	EST	2.8	?
RC_AA425606	AA425606	ESTs Weakly similar to Similar to S.cerevisiae hypothetical protein L3111 [H sapiens]	2.8	TM
RC_AA425900_s	AA425900	Uracil-DNA glycosylase	2.8	other
RC_AA446572	AA446572	EST - RC_AA446572	2.8	other
RC_AA478596	AA478596	ESTs	2.8	?
RC_AA480103	AA480103	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H sapiens]	2.8	TM
RC_AA486407	AA486407	ESTs	2.8	other
RC_AA488432	AA488432	ESTs	2.8	?
RC_AA609200	AA609200	EST - RC_AA609200	2.8	other
RC_AA609501	AA609501	HEAT SHOCK 70 KD PROTEIN 1	2.8	other
AF006516	AF006516	Homo sapiens eps8 binding protein e3B1 mRNA complete cds	2.8	other
RC_D80710_f	D80710	ESTs Weakly similar to transmembrane protein [H sapiens]	2.8	?
RC_F03605_f	F03605	PUTATIVE 60S RIBOSOMAL PROTEIN	2.8	other
RC_H24460_s	H24460	FK506-binding protein 4 (59kD)	2.8	other
RC_N21159	N21159	Homo sapiens forkhead protein (FKHRL1) mRNA complete cds	2.8	other
RC_N29325	N29325	ESTs Highly similar to 47 KD PROTEIN [Pseudomonas chlororaphis]	2.8	other
RC_N48715	N48715	ESTs	2.8	SS,TM
RC_N92915	N92915	ESTs	2.8	other
RC_R39234_r	R39234	ESTs Weakly similar to elastin like protein [D melanogaster]	2.8	TM
RC_R41933	R41933	ESTs	2.8	?
RC_R46025	R46025	ESTs	2.8	SS,
RC_R49327	R49327	Natural resistance-associated macrophage protein 2	2.8	TM
RC_R79617	R79617	ESTs	2.8	other
RC_T63857	T63857	EST - RC_T63857	2.8	?
U30825	U30825	Human splicing factor SRp30c mRNA complete cds	2.8	other
U53347	U53347	Human neutral amino acid transporter B mRNA complete cds	2.8	TM
X76732	X76732	DNA-BINDING PROTEIN NEFA PRECURSOR	2.8	SS,
RC_AA102520	AA102520	ESTs Highly similar to HYPOTHETICAL 31.6 KD PROTEIN F54F2.9 IN CHROMOSOME III [Caenorhabditis elegans]	2.7	TM
RC_AA125969	AA125969	ESTs Weakly similar to F35G12.9 [C.elegans]	2.7	?
RC_AA126743	AA126743	ESTs	2.7	other
RC_AA164687	AA164687	ESTs	2.7	other
AA215333	AA215333	ESTs	2.7	TM
RC_AA291269	AA291269	ESTs	2.7	other
RC_AA424031	AA424031	ESTs	2.7	other
RC_AA425725	AA425725	ESTs Weakly similar to serine protein kinase SRPK1 [H sapiens]	2.7	other
RC_AA431333_s	AA431333	ESTs Highly similar to Ras inhibitor [H.sapiens]	2.7	other
RC_AA449718	AA449718	ESTs Weakly similar to ZINC FINGER PROTEIN 42 [H sapiens]	2.7	other
RC_AA461509	AA461509	ESTs Weakly similar to putative p150 [H.sapiens]	2.7	other
RC_AA620586	AA620586	ESTs	2.7	?
D63391	D63391	Human mRNA for platelet activating factor acetylhydrolase IB gamma-subunit complete cds	2.7	other
RC_F02863	F02863	ESTs Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H sapiens]	2.7	TM
K02777	K02777	T cell receptor alpha-chain	2.7	TM
L11669	L11669	Human tetracycline transporter-like protein mRNA complete cds	2.7	SS,TM
L12350	L12350	Thrombospondin 2	2.7	other
M96982	M96982	SPLICING FACTOR U2AF 35 KD SUBUNIT	2.7	?
RC_N23663	N23663	ESTs	2.7	other
RC_N25798	N25798	ESTs	2.7	TM
RC_R02354	R02354	ESTs	2.7	other
RC_R54112	R54112	ESTs	2.7	other
RC_R71481	R71481	ESTs	2.7	TM
U33052	U33052	Human lipid-activated protein kinase PRK2 mRNA complete cds	2.7	other

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RC_W69160	W69160	ESTs	2.7	other
RC_W80750	W80750	ESTs	2.7	other
RC_W87747	W87747	ESTs	2.7	other
X16396	X16396	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE	2.7	SS.
X89986	X89986	H sapiens mRNA for NBK apoptotic inducer protein	2.7	TM
RC_AA001402	AA001402	Homo sapiens 15 kDa selenoprotein mRNA complete cds	2.6	other
RC_AA176121	AA176121	ESTs	2.6	other
RC_AA242758_s	AA242758	Human breast cancer estrogen regulated LIV-1 protein (LIV-1) mRNA partial cds	2.6	SS,TM
RC_AA293300_s	AA293300	ESTs Weakly similar to semaphorin C [M.musculus]	2.6	SS.
RC_AA412112	AA412112	EST - RC_AA412112	2.6	?
RC_AA417956	AA417956	ESTs	2.6	other
RC_AA447553	AA447553	ESTs	2.6	other
RC_AA447617	AA447617	ESTs	2.6	other
RC_AA453624	AA453624	Human terminal transferase mRNA complete cds	2.6	other
RC_AA598648_s	AA598648	Human mRNA for transcriptional activator hSNF2b complete cds	2.6	other
AB000115	AB000115	Homo sapiens mRNA expressed in osteoblast complete cds	2.6	other
AF001294	AF001294	Homo sapiens IPL (IPL) mRNA complete cds	2.6	SS.
D63881	D63881	Human mRNA for KIAA0160 gene partial cds	2.6	TM
D79997	D79997	Human mRNA for KIAA0175 gene complete cds	2.6	TM
RC_H98655	H98655	Homo sapiens nibrin (NBS) mRNA complete cds	2.6	other
L03411	L03411	Radin blood group	2.6	other
L04490	L04490	Homo sapiens (clone CC6) NADH-ubiquinone oxidoreductase subunit mRNA 3' end cds	2.6	TM
RC_N33516	N33516	Homo sapiens nibrin (NBS) mRNA complete cds	2.6	TM
RC_N46252	N46252	ESTs	2.6	other
RC_N48790	N48790	ESTs Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	2.6	other
RC_N51316	N51316	ESTs Highly similar to elastin like protein [D.melanogaster]	2.6	other
RC_N63210	N63210	ESTs	2.6	other
RC_N68869	N68869	ESTs	2.6	other
RC_N92948_s	N92948	Human IEF SSP 9502 mRNA complete cds	2.6	?
RC_R50333_i	R50333	ESTs	2.6	SS,TM
T39176_s	T39176	ESTs Weakly similar to ZK1058.4 [C.elegans]	2.6	TM
RC_W85712	W85712	ESTs Weakly similar to PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR [H.sapiens]	2.6	other
Z49099	Z49099	H sapiens mRNA for spermine synthase	2.5	other
RC_AA045083	AA045083	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE	2.5	other
RC_AA069547	AA069547	EST - RC_AA069547	2.5	?
RC_AA130349	AA130349	ESTs	2.5	other
RC_AA160890_s	AA160890	Human mRNA for KIAA0389 gene complete cds	2.5	other
RC_AA191424	AA191424	ESTs	2.5	other
RC_AA236489	AA236489	ESTs	2.5	other
RC_AA251587	AA251587	Homo sapiens mRNA for KIAA0530 protein partial cds	2.5	other
RC_AA262491	AA262491	ESTs	2.5	?
RC_AA262730	AA262730	ESTs	2.5	other
RC_AA284372	AA284372	ESTs	2.5	?
RC_AA291503	AA291503	EST	2.5	SS.
RC_AA369027	AA369027	ESTs	2.5	other
RC_AA398280	AA398280	ESTs	2.5	other
RC_AA404957	AA404957	Matrix Gla protein	2.5	other
RC_AA416877	AA416877	ESTs	2.5	?
RC_AA428179	AA428179	EST	2.5	other
RC_AA446100	AA446100	ESTs	2.5	other
RC_AA451707	AA451707	ESTs	2.5	other
RC_AA490882_s	AA490882	ESTs	2.5	other
RC_AA610073	AA610073	ESTs	2.5	other
AB002308	AB002308	Human mRNA for KIAA0310 gene complete cds	2.5	TM
D43948	D43948	Human mRNA for KIAA0097 gene complete cds	2.5	other
RC_D60374_f	D60374	EST - RC_D60374_f	2.5	other
RC_H12634	H12634	ESTs	2.5	?
L00205	L00205	KERATIN TYPE II CYTOSKELETAL 6D	2.5	TM
M23379	M23379	GTPase-activating protein ras p21 (RASA)	2.5	other
RC_N21677	N21677	ESTs	2.5	TM
RC_N66158	N66158	ESTs	2.5	other
RC_N67187_s	N67187	ESTs	2.5	TM
RC_N70646	N70646	ESTs		

FIGURE 7 (cont.)

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RC_N93000	N93000	ESTs	2.5	other
T39763_s	T39763	ESTs	2.5	other
RC_T70541	T70541	ESTs	2.5	SS,
U16306	U16306	LARGE FIBROBLAST PROTEOGLYCAN PRECURSOR	2.5	SS,
RC_W47183	W47183	ESTs	2.5	other
X54941	X54941	CDC28 protein kinase 1	2 5	other
X70218	X70218	Protein phosphatase 4 (formerly X) catalytic subunit	2.5	other
X85373	X85373	H sapiens mRNA for Sm protein G	2.5	other
RC_AA039887	AA039887	ESTs	2.4	other
RC_AA147708	AA147708	ESTs Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]	2 4	other
RC_AA190993	AA190993	ESTs	2.4	other
RC_AA218663	AA218663	ESTs Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]	2.4	other
RC_AA223209	AA223209	ESTs Weakly similar to D9481.16 gene product [S.cerevisiae]	2 4	other
RC_AA252672_s	AA252672	Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds	2 4	other
RC_AA258601	AA258601	EST - RC_AA258601	2.4	?
RC_AA262651	AA262651	ESTs	2 4	other
RC_AA279799	AA279799	ESTs	2 4	other
RC_AA286942	AA286942	EST - RC_AA286942	2 4	?
RC_AA371604	AA371604	Human Rho-associated coiled-coil containing protein kinase p160ROCK mRNA complete cds	2 4	other
RC_AA399047	AA399047	ESTs	2 4	other
AA434329	AA434329	ESTs	2 4	other
RC_AA449458	AA449458	ESTs	2.4	TM
RC_AA455239	AA455239	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 [Caenorhabditis elegans]	2 4	other
RC_AA456646	AA456646	ESTs	2 4	other
RC_AA487207	AA487207	EST - RC_AA487207	2 4	other
AA504223	AA504223	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 [Caenorhabditis elegans]	2 4	other
RC_AA599674	AA599674	ESTs Weakly similar to F08G12.1 [C.elegans]	2 4	SS,
D38555	D38555	Human mRNA for KIAA0079 gene complete cds	2 4	other
D82348	D82348	Human mRNA for 5-aminoimidazole-4-carboxamide-1-beta-D-ribonucleotide transformylase/inosinicase complete cds	2.4	other
D87684	D87684	Human mRNA for KIAA0242 gene partial cds	2 4	other
M55542	M55542	Guanylate binding protein 1 interferon-inducible 67kD	2.4	TM
M90516	M90516	Glutamine-fructose-6-phosphate transaminase	2 4	TM
RC_N51260_s	N51260	Human mRNA for KIAA0240 gene partial cds	2 4	other
RC_N69352	N69352	Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds	2 4	other
RC_R37778	R37778	ESTs	2.4	other
S82597_ma1	S82597	H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)	2 4	?
RC_T25896	T25896	ESTs	2 4	other
RC_T29681_f	T29681	Human serine kinase mRNA complete cds	2 4	other
U73477	U73477	HLA-DR ASSOCIATED PROTEIN I	2 4	other
RC_W31919	W31919	EST	2 4	other
W79060	W79060	ESTs Highly similar to ribosome-binding protein p34 [R norvegicus]	2 4	other
X13482	X13482	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'	2 4	other
X60382_ma1	X60382	COL10A1	2 4	?
X84373	X84373	NUCLEAR FACTOR RIP140	2 4	other
RC_Z40898	Z40898	ESTs	2 4	other
RC_AA010065_s	AA010065	CDC28 protein kinase 2	2 3	other
RC_AA024658	AA024658	ESTs	2 3	SS,TM
RC_AA031814	AA031814	ESTs Weakly similar to R01H10 8 [C.elegans]	2 3	?
RC_AA037410_s	AA037410	Human DNA sequence from PAC 127B20 on chromosome 22q11 2-qter contains GTPase-activating protein similar to rhoGAP protein ribosomal protein L6 pseudogene ESTs and CA repeat	2 3	other
RC_AA037657_s	AA037657	ESTs	2 3	TM
RC_AA069285	AA069285	ESTs Weakly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 [C.elegans]	2 3	other
RC_AA173223	AA173223	ESTs	2.3	other
RC_AA236951_s	AA236951	ESTs	2 3	other
RC_AA250737	AA250737	ESTs	2.3	other
RC_AA251776	AA251776	ESTs	2 3	other
RC_AA282568	AA282568	ESTs Weakly similar to F25H2.6 [C.elegans]	2.3	other
AA330771_s	AA330771	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence	2 3	TM
RC_AA425749	AA425749	ESTs	2 3	TM
RC_AA428647	AA428647	ESTs	2 3	other
RC_AA450116	AA450116	ESTs	2 3	other

FIGURE 7 (cont.)
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RC_AA459673	AA459673	ESTs Highly similar to CHROMOSOME SEGREGATION PROTEIN CUT3 [Schizosaccharomyces pombe]	2 3	other
RC_AA464423	AA464423	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	2 3	other
D00591	D00591	Chromosome condensation 1	2 3	?
D26156	D26156	Human mRNA for transcriptional activator hSNF2b complete cds	2.3	other
RC_F02907	F02907	ESTs	2.3	other
J05633	J05633	Integnn beta-5 subunit	2.3	TM
RC_N29888	N29888	Human NAD+-specific isocitrate dehydrogenase beta subunit precursor mRNA nuclear gene encoding mitochondrial protein complete cds	2.3	SS,TM
RC_N33063	N33063	ESTs Highly similar to GAG POLYPROTEIN [Avian spleen necrosis virus]	2 3	other
RC_N49284_s	N49284	MYB PROTO-ONCOGENE PROTEIN	2.3	other
RC_N66857	N66857	ESTs	2 3	other
RC_N94581	N94581	ESTs	2.3	?
RC_R52088	R52088	EST - RC_R52088	2.3	TM
RC_R63652	R63652	ESTs	2.3	other
R81830	R81830	Homo sapiens breast cancer putative transcription factor (ZABC1) mRNA complete cds	2.3	other
S79873	S79873	Lysosomal-associated membrane protein 2	2.3	other
RC_T87807_s	T87807	ESTs	2.3	SS,TM
U37022_ma1	U37022	Human cyclin-dependent protein kinase mRNA complete cds	2.3	other
U47077	U47077	Human DNA-dependent protein kinase catalytic subunit (DNA-PKcs) mRNA complete cds	2.3	?
U59423	U59423	Human chromosome 4 Mad homolog Smad1 mRNA complete cds	2.3	TM
U72514	U72514	Human C2f mRNA complete cds	2.3	other
U77180	U77180	Human mRNA for EBI1-ligand chemokine complete cds	2.3	other
RC_W23625_s	W23625	ESTs Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION [Saccharomyces cerevisiae]	2.3	TM
RC_W49574	W49574	ESTs Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	2.3	SS,TM
X54199	X54199	Phosphoribosylglycinamide formyltransferase phosphoribosylglycinamide synthetase phosphoribosylaminoimidazole synthetase	2.3	other
X94453	X94453	Pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)	2.3	?
RC_Z39909	Z39909	ESTs Moderately similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]	2.3	other
Z48042	Z48042	H sapiens mRNA encoding GPI-anchored protein p137	2.3	other
RC_AA011556	AA011556	ESTs	2.2	other
RC_AA028028	AA028028	ESTs	2 2	other
AA043160	AA043160	ESTs	2 2	other
RC_AA043353_s	AA043353	ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]	2 2	other
RC_AA053636	AA053636	ESTs	2.2	other
RC_AA059214	AA059214	ESTs Moderately similar to neurexophilin 2 [M.musculus]	2 2	SS,
RC_AA076328_s	AA076328	Cyclin-dependent kinase inhibitor 2A (melanoma p16 inhibits CDK4)	2.2	TM
RC_AA126719	AA126719	ESTs	2.2	other
RC_AA131692	AA131692	ESTs	2.2	other
RC_AA148516	AA148516	ESTs	2 2	other
RC_AA150088	AA150088	Homo sapiens vesicle transport related protein mRNA partial cds	2 2	TM
RC_AA227856	AA227856	H.sapiens mRNA for HOXC9 protein exon 1	2.2	other
RC_AA236516	AA236516	ESTs Weakly similar to ISOLEUCYL-TRNA SYNTHETASE MITOCHONDRIAL [S.cerevisiae]	2 2	other
RC_AA251766	AA251766	ESTs Moderately similar to metastasis-associated gene [H sapiens]	2 2	other
RC_AA280588	AA280588	ESTs	2 2	other
RC_AA287320	AA287320	ESTs	2 2	other
RC_AA287833	AA287833	ESTs	2.2	other
RC_AA397921	AA397921	Homo sapiens mRNA transcriptional unit N143	2.2	other
RC_AA416735	AA416735	ESTs	2 2	TM
RC_AA417030	AA417030	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds	2.2	other
RC_AA423827_f	AA423827	ESTs	2 2	other
RC_AA430726	AA430726	EST - RC_AA430726	2 2	SS,
RC_AA436477	AA436477	ESTs	2 2	TM
RC_AA436613	AA436613	ESTs	2 2	other
RC_AA446949	AA446949	ESTs	2.2	other
RC_AA485223	AA485223	ESTs	2 2	TM
RC_AA490237	AA490237	EST - RC_AA490237	2 2	other
RC_AA495924	AA495924	ESTs	2 2	other
RC_AA600200	AA600200	ESTs	2.2	SS,
RC_D80237_s	D80237	Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA complete cds	2.2	?
RC_F09328	F09328	ESTs	2 2	other
RC_F13690_s	F13690	ESTs Weakly similar to ZNF127-Xp [H.sapiens]	2 2	other
RC_H28428	H28428	ESTs	2 2	other
RC_H84658_s	H84658	ESTs	2 2	other

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RC_H99261_s	H99261	Human DNA from overlapping chromosome 19 cosmids R31396 F25451 and R31076 containing COX6B and UPKA genomic sequence	2.2	TM
RC_N39148	N39148	ESTs	2 2	other
RC_N90401	N90401	ESTs	2 2	TM
RC_N93618	N93618	ESTs	2 2	other
RC_N94606	N94606	ESTs	2 2	other
RC_R72008	R72008	ESTs Weakly similar to Dif33 gene product (H.sapiens)	2.2	other
R78119	R78119	ESTs	2.2	other
RC_T10060	T10060	ESTs	2 2	TM
RC_T15674_f	T15674	ESTs	2.2	?
RC_T59686_s	T59686	ESTs	2.2	other
U09510	U09510	Glycyl-tRNA synthetase	2.2	other
U09770	U09770	Human cysteine-rich heart protein (hCRHP) mRNA complete cds	2.2	SS,TM
U86782	U86782	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds	2.2	other
X70476	X70476	COATOMER BETA' SUBUNIT	2.2	?
RC_AA018587	AA018587	ESTs Weakly similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! (H.sapiens)	2 1	?
RC_AA134063	AA134063	ESTs	2.1	other
RC_AA158132	AA158132	ESTs Highly similar to YSA1 PROTEIN (Saccharomyces cerevisiae)	2.1	other
RC_AA251909	AA251909	Homo sapiens MAD3-like protein kinase mRNA complete cds	2.1	other
RC_AA253031	AA253031	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds	2.1	other
RC_AA281780	AA281780	ESTs Weakly similar to HYPOTHETICAL 46 4 KD PROTEIN T16H12.5 IN CHROMOSOME III (C.elegans)	2.1	other
RC_AA291137	AA291137	ESTs	2.1	other
RC_AA393695	AA393695	LARGE FIBROBLAST PROTEOGLYCAN PRECURSOR	2 1	other
RC_AA400820_s	AA400820	ESTs	2 1	other
RC_AA403121	AA403121	ESTs	2.1	SS,
RC_AA426060	AA426060	ESTs	2 1	other
RC_AA427662	AA427662	ESTs	2 1	other
RC_AA451712	AA451712	ESTs	2 1	other
AA460077	AA460077	ESTs	2 1	other
RC_AA465148	AA465148	ESTs	2 1	other
RC_AA609869	AA609869	ESTs	2 1	other
RC_AA610039	AA610039	ESTs	2 1	other
RC_AA620464	AA620464	Human mRNA for KIAA0331 gene complete cds	2 1	?
D13988	D13988	Homo sapiens mRNA for GDP dissociation inhibitor beta	2.1	TM
RC_F01986_f	F01986	EST	2 1	?
RC_H38246_s	H38246	ESTs Weakly similar to similar to S. cerevisiae LAG1 (C elegans)	2.1	TM
RC_H80737_s	H80737	ESTs	2 1	TM
M30938	M30938	ATP-DEPENDENT DNA HELICASE II 86 KD SUBUNIT	2 1	other
M74099	M74099	Cut (Drosophila)-like 1 (CCAAT displacement protein)	2.1	?
RC_N22222	N22222	ESTs	2 1	other
RC_N24968	N24968	Homo sapiens vacuolar H(+)-ATPase subunit mRNA complete cds	2 1	other
RC_N64378	N64378	ESTs	2 1	other
RC_N72113	N72113	ESTs	2 1	other
RC_N95837	N95837	Homo sapiens clone 24651 mRNA sequence	2 1	TM
RC_R91380_s	R91380	H sapiens RNA for CLCN3	2 1	TM
U51205	U51205	Human COP9 homolog (HCOP9) mRNA complete cds	2 1	other
U58090	U58090	Human Hs-cul-4A mRNA partial cds	2 1	other
U60808	U60808	Human CDP-diacylglycerol synthase (CDS) mRNA complete cds	2 1	TM
U61232	U61232	Human tubulin-folding cofactor E mRNA complete cds	2 1	other
U67122	U67122	Human ubiquitin-homology domain protein PIC1 mRNA complete cds	2 1	other
RC_W20391_s	W20391	Human mRNA for kinesin-related protein partial cds	2 1	other
RC_W32470	W32470	ESTs	2 1	other
RC_W37384_i	W37384	Homo sapiens testis-specific nm23 homolog mRNA complete cds	2 1	other
X70683	X70683	SRY (sex determining region Y)-box 4	2 1	TM
X70944	X70944	PTB-ASSOCIATED SPLICING FACTOR	2 1	other
RC_Z99394_s	Z99394	ESTs Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! (H sapiens)	2 1	other
RC_AA045481	AA045481	ESTs	2	TM
RC_AA047265	AA047265	Homo sapiens mRNA for osteoblast specific cysteine-rich protein complete cds	2	SS,
RC_AA127716	AA127716	Homo sapiens unknown mRNA complete cds	2	TM
RC_AA136884	AA136884	ESTs	2	other
RC_AA181657	AA181657	ESTs	2	other
RC_AA188981	AA188981	Homo sapiens retinoblastoma-associated protein HEC mRNA complete cds	2	?
RC_AA233177	AA233177	ESTs	2	other
RC_AA237022	AA237022	ESTs	2	other

FIGURE 7 (cont.)

RC_AA287388	AA287388	ESTs	2	other
RC_AA405838	AA405838	ESTs	2	other
RC_AA417909	AA417909	ESTs	2	other
RC_AA426375	AA426375	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]	2	other
AA443460	AA443460	ESTs	2	other
RC_AA443596	AA443596	ESTs	2	other
RC_AA453255	AA453255	ESTs	2	other
RC_AA476312	AA476312	ESTs	2	TM
RC_AA476582	AA476582	ESTs Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT [Mus musculus]	2	other
RC_AA479139_s	AA479139	Acid phosphatase 1 soluble	2	other
RC_AA487202	AA487202	ESTs	2	other
RC_AA521474	AA521474	ESTs	2	?
RC_AA598452	AA598452	ESTs	2	other
RC_AA621122	AA621122	ESTs	2	other
AF015913	AF015913	Homo sapiens SKB1Hs mRNA complete cds	2	other
D28364	D28364	EST - D28364	2	other
RC_D53392_f	D53392	ESTs Weakly similar to PEREGRIN [H.sapiens]	2	TM
D78586	D78586	CAD PROTEIN	2	other
D80000	D80000	Human mRNA for KIAA0178 gene partial cds	2	TM
D86978	D86978	Human mRNA for KIAA0225 gene partial cds	2	other
RC_F02651	F02651	ESTs	2	other
RC_H11938	H11938	EST - RC_H11938	2	other
RC_H78241_s	H78241	H.sapiens mRNA for novel member of serine-arginine domain protein SRrp129	2	other
L20298	L20298	Core-binding factor beta subunit	2	TM
L37347	L37347	Natural resistance-associated macrophage protein 2	2	TM
M23263	M23263	Androgen receptor (dihydrotestosterone receptor testicular feminization spinal and bulbar muscular atrophy Kennedy disease)	2	other
RC_N22162	N22162	ESTs	2	other
RC_N24954	N24954	ESTs	2	TM
RC_N50963	N50963	ESTs	2	SS.
RC_N70520	N70520	ESTs	2	?
RC_N91246	N91246	ESTs	2	?
RC_R68425	R68425	ESTs	2	TM
RC_R73567	R73567	Homo sapiens meltrin-L precursor (ADAM12) mRNA complete cds	2	other
RC_T23539	T23539	ESTs Highly similar to zinc finger protein [M musculus]	2	?
T63174_s	T63174	ESTs	2	other
RC_T90746	T90746	ESTs	2	other
U05340	U05340	Human p55CDC mRNA complete cds	2	other
U34044	U34044	Human selenium donor protein (selD) mRNA complete cds	2	TM
U37519	U37519	Aldehyde dehydrogenase 8	2	other
U39840	U39840	Human hepatocyte nuclear factor-3 alpha (HNF-3 alpha) mRNA complete cds	2	other
U91932	U91932	Human mRNA for clathrin coat assembly protein-like complete cds	2	other
W28362	W28362	ESTs	2	other
RC_W80467	W80467	ESTs	2	other
X69636	X69636	Human mRNA for KIAA0393 gene complete cds	2	other
X92896	X92896	H sapiens mRNA for ITBA2 protein	2	?
Z24724	Z24724	H.sapiens polyA site DNA	2	other
Z29090	Z29090	PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT ALPHA ISOFORM	2	other
RC_Z39053	Z39053	ESTs	2	TM
RC_Z40810	Z40810	ESTs	2	?
Z47727	Z47727	H.sapiens mRNA for RNA polymerase II subunit	1.9	TM
RC_AA112679	AA112679	ESTs	1.9	other
AA115058_s	AA115058	ESTs	1.9	other
RC_AA149585	AA149585	ESTs	1.9	other
RC_AA173417	AA173417	ESTs	1.9	?
RC_AA227463	AA227463	ESTs Weakly similar to No definition line found [C.elegans]	1.9	TM
RC_AA227963	AA227963	ESTs	1.9	TM
RC_AA233168	AA233168	ESTs Highly similar to HYPOTHETICAL 16.5 KD PROTEIN IN PAS8-EGT2 INTERGENIC REGION [Saccharomyces cerevisiae]	1.9	other
RC_AA233261	AA233261	ESTs	1.9	other
RC_AA236453	AA236453	ESTs	1.9	other
RC_AA257972	AA257972	ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]	1.9	other
RC_AA278653_f	AA278653	ESTs	1.9	other
RC_AA287834	AA287834	ESTs		

FIGURE 7 (cont.)

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RC_AA302745	AA302745	ESTs	1.9	?
RC_AA403008	AA403008	ESTs	1.9	?
RC_AA446918	AA446918	EST	1.9	?
RC_AA451898	AA451898	ESTs	1.9	other
AA464013	AA464013	ESTs Weakly similar to Y53C12A.3 [C.elegans]	1.9	TM
RC_AA489046	AA489046	ESTs	1.9	TM
RC_AA496000	AA496000	ESTs	1.9	SS.
RC_AA497052	AA497052	ESTs	1.9	other
RC_AA504832	AA504832	ESTs Weakly similar to Sp140 protein [H.sapiens]	1.9	other
D12485	D12485	PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1	1.9	TM
D13645	D13645	Human mRNA for KIAA0020 gene complete cds	1.9	other
D50920	D50920	Homo sapiens thyroid hormone receptor-associated protein complex component TRAP100 mRNA complete cds	1.9	TM
H44386_s	H44386	ESTs	1.9	other
L13689	L13689	Murine leukemia viral (bmi-1) oncogene homolog	1.9	other
L33801	L33801	Human protein kinase mRNA complete cds	1.9	other
M21259	M21259	Small nuclear ribonucleoprotein polypeptide E	1.9	?
RC_N23393	N23393	ESTs	1.9	other
RC_N46423	N46423	ESTs	1.9	other
RC_N47469	N47469	ESTs	1.9	other
RC_N55336	N55336	ESTs	1.9	TM
RC_T25867	T25867	EST	1.9	?
RC_T77464	T77464	H.sapiens mRNA for transcriptional intermediary factor 2	1.9	other
RC_T89703	T89703	ESTs Weakly similar to siah binding protein 1 [H.sapiens]	1.9	other
HG174-HT174	TIGR - HG174-HT174	EST - HG174-HT174	1.9	?
U05237	U05237	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA complete cds	1.9	other
U26312	U26312	Human heterochromatin protein HP1Hs-gamma mRNA complete cds	1.9	other
U41387	U41387	Human Gu protein mRNA partial cds	1.9	other
U76638	U76638	Human BRCA1-associated RING domain protein (BARD1) mRNA complete cds	1.9	other
RC_W37933	W37933	EST - RC_W37933	1.9	?
RC_W80763	W80763	ESTs Highly similar to FK506-BINDING PROTEIN PRECURSOR [Mus musculus]	1.9	other
RC_W95063	W95063	ESTs Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME I [Schizosaccharomyces pombe]	1.9	TM
X12791	X12791	Signal recognition particle 19 kD protein	1.9	other
X55448_cds1	X55448	H.sapiens mRNA for 2.19 gene	1.9	?
X58072	X58072	GATA-binding protein 3	1.9	other
X81788	X81788	Homo sapiens ICT1 (alias DS-1) mRNA	1.9	other
X82153	X82153	CATHEPSIN K PRECURSOR	1.9	other
RC_Z40715	Z40715	ESTs Weakly similar to T13F2.1 [C.elegans]	1.9	TM
RC_AA005108	AA005108	ESTs	1.8	other
RC_AA028074	AA028074	ESTs	1.8	other
RC_AA063460_s	AA063460	Gastrin-releasing peptide	1.8	SS.
AA099241	AA099241	ESTs Moderately similar to 60S RIBOSOMAL PROTEIN L29 [H.sapiens]	1.8	other
RC_AA131584	AA131584	ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]	1.8	other
RC_AA191353	AA191353	ESTs	1.8	TM
RC_AA232103	AA232103	ESTs	1.8	other
RC_AA232104	AA232104	ESTs Highly similar to transcription factor ARF6 chain B [M.musculus]	1.8	other
RC_AA234765	AA234765	ESTs	1.8	TM
RC_AA251758	AA251758	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA complete cds	1.8	other
RC_AA251982	AA251982	Homo sapiens clone 23770 mRNA sequence	1.8	other
RC_AA279171	AA279171	ESTs Weakly similar to F25D7.1 [C.elegans]	1.8	other
RC_AA283743_s	AA283743	ESTs Moderately similar to YY1-associated factor 2 [H.sapiens]	1.8	other
RC_AA291923	AA291923	ESTs	1.8	TM
RC_AA292066_i	AA292066	ESTs Weakly similar to C01H6.7 [C.elegans]	1.8	TM
RC_AA398319	AA398319	ESTs	1.8	other
RC_AA401274	AA401274	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds	1.8	other
RC_AA406478	AA406478	ESTs	1.8	TM
RC_AA411144	AA411144	ESTs	1.8	TM
RC_AA417962	AA417962	ESTs Highly similar to GERANYLGERANYL PYROPHOSPHATE SYNTHETASE [Neurospora crassa]	1.8	other
RC_AA420988	AA420988	ESTs	1.8	other
RC_AA436171	AA436171	ESTs	1.8	other
RC_AA436192	AA436192	ESTs	1.8	other
RC_AA447603	AA447603	EST	1.8	?
AA455001_s	AA455001	ESTs	1.8	other

FIGURE 7 (cont.)

RC_AA457566	AA457566	ESTs	1.8	other
RC_AA460350	AA460350	ESTs	1.8	other
RC_AA598988	AA598988	ESTs Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION [Saccharomyces cerevisiae]	1.8	SS,
RC_AA599219	AA599219	ESTs Moderately similar to ALR [H.sapiens]	1.8	other
AF000430	AF000430	Homo sapiens mRNA for Dnm1p/Vps1p-like protein complete cds	1.8	TM
D13630	D13630	Human mRNA for KIAA0005 gene complete cds	1.8	other
RC_D59894	D59894	ESTs	1.8	other
RC_F02990	F02990	ESTs Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]	1.8	other
RC_F04989	F04989	ESTs	1.8	other
RC_H94248	H94248	ESTs	1.8	other
L10910	L10910	Homo sapiens splicing factor (CC1.3) mRNA complete cds	1.8	other
L25876	L25876	Human protein phosphatase (KAP1) mRNA complete cds	1.8	other
L76937_ma1	L76937	Homo sapiens Werner syndrome gene complete cds	1.8	?
M36429	M36429	Human transducin beta-2 subunit mRNA complete cds	1.8	other
M63180	M63180	Threonyl-tRNA synthetase	1.8	other
RC_N26855	N26855	ESTs Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	1.8	other
RC_N35583	N35583	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58]	1.8	?
RC_N50050	N50050	ESTs	1.8	other
RC_N52006	N52006	ESTs	1.8	TM
RC_R41281	R41281	Homo sapiens DNJ3/CPR3 mRNA complete cds	1.8	other
RC_T96595	T96595	EST - RC_T96595	1.8	TM
U14518	U14518	Centromere protein A (17kD)	1.8	other
U32986	U32986	Damage-specific DNA binding protein 1 (127 kD)	1.8	TM
U65928	U65928	V-jun avian sarcoma virus 17 oncogene homolog	1.8	other
U70322	U70322	Human transportin (TRN) mRNA complete cds	1.8	other
U72263	U72263	Exostoses (multiple) 2	1.8	TM
RC_W52225	W52225	ESTs	1.8	other
W68502	W68502	ESTs	1.8	other
RC_W72876	W72876	ESTs	1.8	SS,
RC_W84790_s	W84790	Human mRNA for KIAA0208 gene complete cds	1.8	?
RC_W88983	W88983	Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA complete cds	1.8	other
X65488	X65488	HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U	1.8	other
X75962	X75962	OX40L RECEPTOR PRECURSOR	1.8	SS,TM
X92098	X92098	H.sapiens mRNA for transmembrane protein mp24	1.8	SS,TM
RC_Z40332	Z40332	Homo sapiens mRNA for p115 complete cds	1.8	other
RC_AA035143	AA035143	ESTs	1.7	other
RC_AA056249	AA056249	Collagen type IV alpha 3	1.7	other
RC_AA056588	AA056588	ESTs	1.7	other
RC_AA111879	AA111879	EST	1.7	?
RC_AA116075	AA116075	ESTs	1.7	other
RC_AA132514	AA132514	Homo sapiens drp1 mRNA complete cds	1.7	other
RC_AA156142_s	AA156142	ESTs	1.7	TM
RC_AA171529	AA171529	ESTs	1.7	TM
RC_AA180321	AA180321	ESTs Weakly similar to W04D2.6 [C.elegans]	1.7	other
RC_AA232315	AA232315	Homo sapiens clone 23797 and 23917 mRNA partial cds	1.7	other
RC_AA234767	AA234767	ESTs	1.7	TM
RC_AA262957	AA262957	ESTs	1.7	TM
RC_AA280687	AA280687	ESTs	1.7	other
RC_AA286891	AA286891	ESTs	1.7	other
RC_AA287091_s	AA287091	ESTs Highly similar to C10 [H.sapiens]	1.7	other
RC_AA291260	AA291260	ESTs	1.7	other
RC_AA400080	AA400080	EST	1.7	?
RC_AA410894	AA410894	ESTs	1.7	other
RC_AA410972	AA410972	ESTs	1.7	other
RC_AA416733	AA416733	ESTs	1.7	TM
RC_AA421773	AA421773	ESTs	1.7	other
RC_AA425439	AA425439	ESTs	1.7	other
RC_AA453465	AA453465	ESTs	1.7	other
RC_AA459005	AA459005	ESTs	1.7	other
RC_AA465690_s	AA465690	Human arginine-rich nuclear protein mRNA complete cds	1.7	other
RC_AA470140	AA470140	ESTs	1.7	?
RC_AA479362	AA479362	ESTs	1.7	SS,
RC_AA479961	AA479961	ESTs	1.7	other

FIGURE 7 (cont.)

RC_AA598447	AA598447	Homo sapiens exportin t mRNA complete cds	1.7	other
RC_AA599267	AA599267	EST - RC_AA599267	1.7	other
RC_AA609053	AA609053	ESTs	1.7	SS,
RC_AA609364	AA609364	EST	1.7	?
AF002668	AF002668	Homo sapiens putative fatty acid desaturase MLD mRNA complete cds	1.7	TM
D31161_s	D31161	ESTs	1.7	TM
D78151	D78151	H.sapiens mRNA for 55.11 binding protein	1.7	TM
RC_H15436	H15436	ESTs	1.7	other
RC_H17620	H17620	ESTs	1.7	TM
RC_H23230	H23230	ESTs	1.7	other
RC_H73608_s	H73608	ESTs	1.7	other
L19161	L19161	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT	1.7	other
L27706	L27706	Chaperonin containing T-complex subunit 6	1.7	?
L76703	L76703	Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA complete cds	1.7	?
RC_N31598	N31598	ESTs	1.7	SS,
RC_N31952	N31952	ESTs Moderately similar to HYPOTHETICAL 66.5 KD PROTEIN F02A9 5 IN CHROMOSOME III [Caenorhabditis elegans]	1.7	other
RC_N50831	N50831	ESTs	1.7	TM
RC_N51226	N51226	ESTs	1.7	other
RC_N58561_s	N58561	Cathepsin B	1.7	other
RC_N90029	N90029	Homo sapiens clone 1400 unknown protein mRNA partial cds	1.7	?
RC_N92860_s	N92860	Proto-oncogene AML1 (alternative products)	1.7	other
RC_R39923	R39923	ESTs	1.7	TM
RC_R93068	R93068	ESTs	1.7	other
RC_T03865	T03865	ESTs	1.7	other
RC_T57317	T57317	ESTs	1.7	?
HG4557-HT4962	TIGR - HG4557-HT4962	EST - HG4557-HT4962	1.7	?
U90551	U90551	Human histone 2A-like protein (H2A/l) mRNA complete cds	1.7	other
U95367	U95367	Human GABA-A receptor pi subunit mRNA complete cds	1.7	TM
RC_W19222	W19222	ESTs	1.7	other
W23469	W23469	Homo sapiens vesicle trafficking protein sec22b mRNA complete cds	1.7	other
RC_W38150	W38150	EST - RC_W38150	1.7	?
W55890	W55890	Human Chromosome 16 BAC clone CIT987SK-A-735G6	1.7	other
RC_W85888	W85888	ESTs	1.7	other
RC_AA026418	AA026418	ESTs	1.6	other
RC_AA099589_s	AA099589	Homo sapiens mRNA for GDP dissociation inhibitor beta	1.6	TM
RC_AA101811	AA101811	EST	1.6	SS,
RC_AA121127	AA121127	ESTs Weakly similar to ZK1058.4 [C.elegans]	1.6	SS,TM
RC_AA148885	AA148885	ESTs	1.6	?
RC_AA151708	AA151708	EST	1.6	other
RC_AA155803	AA155803	ESTs	1.6	other
RC_AA167375	AA167375	Homo sapiens mRNA for KIAA0530 protein partial cds	1.6	other
RC_AA167708	AA167708	ESTs	1.6	other
RC_AA181580_s	AA181580	Homo sapiens importin beta subunit mRNA complete cds	1.6	other
AA187579	AA187579	ESTs Weakly similar to Yel007c-ap [S.cerevisiae]	1.6	other
RC_AA243007	AA243007	ESTs	1.6	?
RC_AA243052	AA243052	ESTs Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [Rattus norvegicus]	1.6	other
RC_AA252360	AA252360	EST	1.6	?
AA256106	AA256106	ESTs	1.6	other
RC_AA256678	AA256678	ESTs Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]	1.6	other
RC_AA258205	AA258205	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA complete cds	1.6	other
RC_AA279667_s	AA279667	Cathepsin B	1.6	other
RC_AA347967	AA347967	ESTs	1.6	other
RC_AA417970	AA417970	ESTs	1.6	SS,
RC_AA424524	AA424524	Homo sapiens mRNA for KIAA0286 gene partial cds	1.6	?
AA426176	AA426176	ESTs Weakly similar to Similar to S.cerevisiae hypothetical protein L3111 [H.sapiens]	1.6	other
RC_AA456437	AA456437	ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT [H.sapiens]	1.6	other
RC_AA456598	AA456598	ESTs	1.6	other
RC_AA463195	AA463195	ESTs	1.6	other
RC_AA465222	AA465222	ESTs	1.6	TM
RC_AA521186	AA521186	ESTs	1.6	TM
RC_AA599622	AA599622	ESTs	1.6	other
AB002343	AB002343	Human mRNA for KIAA0345 gene complete cds	1.6	TM

FIGURE 7 (cont.)

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D14811	D14811	Human mRNA for KIAA0110 gene complete cds	1.6	other
D50840	D50840	Human mRNA for ceramide glucosyltransferase complete cds	1.6	TM
RC_D60856_f	D60856	Homo sapiens UDP-glucose dehydrogenase (UGDH) mRNA complete cds	1.6	other
RC_F03738_f	F03738	ESTs	1.6	other
H19378	H19378	ESTs	1.6	TM
RC_H95039	H95039	Homo sapiens KIAA0442 mRNA partial cds	1.6	other
J03934	J03934	NAD(P)H:menadione oxidoreductase	1.6	other
M22898	M22898	Tumor protein p53 (Li-Fraumeni syndrome)	1.6	?
M34079	M34079	PROBABLE 26S PROTEASE SUBUNIT TBP-1	1.6	other
M97856	M97856	Nuclear autoantigenic sperm protein (histone-binding)	1.6	other
RC_N26259	N26259	ESTs Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 [Paramecium tetraurelia]	1.6	?
RC_N69014_s	N69014	Homo sapiens SOX22 protein (SOX22) mRNA complete cds	1.6	?
RC_N73865	N73865	ESTs Weakly similar to L8004.7 gene product [S.cerevisiae]	1.6	other
RC_R10720	R10720	EST	1.6	?
RC_R15743	R15743	ESTs	1.6	other
R70621	R70621	ESTs Highly similar to hypothetical protein 100K [R.norvegicus]	1.6	?
RC_T23820	T23820	Homo sapiens cyclin T2a mRNA complete cds	1.6	other
RC_T64937_s	T64937	Homo sapiens thyroid receptor interactor (TRIP3) mRNA 3' end of cds	1.6	?
U05237	U05237	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA complete cds	1.6	other
U09820	U09820	X-LINKED HELICASE II	1.6	other
U10323	U10323	Human nuclear factor NF45 mRNA complete cds	1.6	TM
U12424_s	U12424	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	1.6	other
U59286	U59286	Homo sapiens interferon stimulated T-cell alpha chemoattractant precursor mRNA complete cds	1.6	SS,
U61145	U61145	Human enhancer of zeste homolog 2 (EZH2) mRNA complete cds	1.6	other
U76992	U76992	Human Tat-SF1 mRNA complete cds	1.6	other
U90549	U90549	Human non-histone chromosomal protein (NHC) mRNA complete cds	1.6	other
U90909	U90909	Human clone 23722 mRNA sequence	1.6	other
RC_W04698	W04698	ESTs	1.6	other
RC_W15528	W15528	ESTs	1.6	other
W58247_s	W58247	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]	1.6	other
RC_W73820	W73820	ESTs	1.6	other
X53793	X53793	MULTIFUNCTIONAL PROTEIN ADE2	1 6	other
X58521	X58521	NUCLEAR PORE GLYCOPROTEIN P62	1.6	other
X69910	X69910	H.sapiens p63 mRNA for transmembrane protein	1.6	TM
X89059	X89059	H.sapiens mRNA for unknown protein expressed in macrophages	1.6	other
RC_Z38919	Z38919	ESTs	1.6	other
RC_AA041551	AA041551	ESTs	1.5	other
RC_AA056735	AA056735	ESTs Weakly similar to HYPOTHETICAL PROTEIN KIAA0079 [H.sapiens]	1.5	other
AA113913	AA113913	EST - AA113913	1.5	other
RC_AA133309	AA133309	EST	1.5	other
AA146888_s	AA146888	ESTs Highly similar to COATOMER ZETA SUBUNIT [Bos taurus]	1.5	other
AA195179_s	AA195179	ESTs	1.5	other
RC_AA219699	AA219699	ESTs	1.5	other
RC_AA226922	AA226922	ESTs Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]	1.5	?
RC_AA232644_s	AA232644	Protein tyrosine phosphatase non-receptor type 4	1.5	other
RC_AA236672	AA236672	ESTs Weakly similar to DFS70 [H.sapiens]	1.5	?
RC_AA256492	AA256492	ESTs	1.5	other
RC_AA262942	AA262942	ESTs	1.5	other
RC_AA279757	AA279757	ESTs Weakly similar to similar to mouse MMR1 [C.elegans]	1.5	other
RC_AA293568	AA293568	ESTs	1.5	other
RC_AA399550	AA399550	ESTs	1.5	other
RC_AA400271	AA400271	ESTs Highly similar to CALCIUM-TRANSPORTING ATPASE 1 [Saccharomyces cerevisiae]	1.5	TM
RC_AA412528	AA412528	ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [R.norvegicus]	1.5	other
RC_AA433925	AA433925	ESTs	1.5	TM
RC_AA447970	AA447970	EST	1.5	TM
RC_AA476319	AA476319	ESTs	1.5	SS,
RC_AA482014	AA482014	H.sapiens mRNA for centrin gene	1.5	other
RC_AA489086	AA489086	ESTs	1.5	other
RC_AA496257	AA496257	ESTs Weakly similar to DIPEPTIDYL PEPTIDASE IV [H.sapiens]	1.5	other
RC_AA509738	AA509738	ESTs	1.5	other
RC_AA621580	AA621580	ESTs Highly similar to HYPOTHETICAL 66.5 KD PROTEIN IN ADE12-RAP1 INTERGENIC REGION [Saccharomyces cerevisiae]	1.5	other
D31764	D31764	Human mRNA for KIAA0064 gene complete cds	1.5	other

FIGURE 7 (cont.)

D38521	D38521	Human mRNA for KIAA0077 gene partial cds	1.5	other
RC_D51177	D51177	ESTs	1.5	TM
D85418	D85418	Human mRNA for phosphatidylinositol-glycan-class C (PIG-C) complete cds	1.5	TM
L18960	L18960	Eukaryotic translation initiation factor 4C (eIF-4C)	1.5	other
L33881	L33881	Protein kinase C iota	1.5	?
M31523	M31523	Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	1.5	other
M63167	M63167	V-akt murine thymoma viral oncogene homolog 1	1.5	other
RC_N21978	N21978	ESTs	1.5	other
RC_N26101	N26101	ESTs Weakly similar to DPY-30 PROTEIN [C.elegans]	1.5	other
RC_N37065	N37065	ESTs	1.5	other
RC_N48677	N48677	ESTs	1.5	TM
RC_N52271	N52271	Homo sapiens LIM protein mRNA complete cds	1.5	other
RC_N54450_i	N54450	ESTs	1.5	?
RC_N67390	N67390	ESTs	1.5	TM
RC_N68640	N68640	ESTs	1.5	other
RC_N78717_s	N78717	H.sapiens mRNA for translin	1.5	?
RC_R07016	R07016	ESTs	1.5	other
RC_R87660	R87660	EST - RC_R87660	1.5	TM
RC_T10258	T10258	EST	1.5	?
RC_T98843	T98843	ESTs Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	1.5	TM
HG884-HT884	TIGR - HG884-HT884	EST - HG884-HT884	1.5	?
U09564	U09564	Human serine kinase mRNA complete cds	1.5	other
U35451	U35451	Homo sapiens heterochromatin protein p25 mRNA complete cds	1.5	?
U41668	U41668	Deoxyguanosine kinase	1.5	other
U50939	U50939	Human amyloid precursor protein-binding protein 1 mRNA complete cds	1.5	other
U94836	U94836	Human ERPROT 213-21 mRNA complete cds	1.5	other
W28366	W28366	Homo sapiens clone 24800 mRNA sequence	1.5	other
RC_W72138	W72138	Homo sapiens putative transcriptional repressor E2F-6 mRNA partial cds	1.5	other
RC_W93640	W93640	ESTs	1.5	other
RC_Z39211	Z39211	Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA complete cds	1.5	other
RC_Z39255_f	Z39255	ESTs	1.5	other
RC_AA025086	AA025086	ESTs	1.4	other
RC_AA057193	AA057193	ESTs	1.4	other
RC_AA085918	AA085918	H.sapiens HUNKI mRNA	1.4	other
RC_AA114250_s	AA114250	Homo sapiens mRNA for KIAA0512 protein complete cds	1.4	other
RC_AA135095	AA135095	Homo sapiens Sox-like transcriptional factor mRNA complete cds	1.4	other
RC_AA156542	AA156542	ESTs	1.4	other
RC_AA171939	AA171939	ESTs	1.4	other
RC_AA195515	AA195515	ESTs	1.4	TM
RC_AA255554	AA255554	ESTs	1.4	TM
RC_AA262943	AA262943	ESTs	1.4	other
RC_AA278755	AA278755	ESTs Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]	1.4	other
RC_AA279991	AA279991	ESTs	1.4	other
AA285277	AA285277	Homo sapiens brain expressed ring finger protein mRNA complete cds	1.4	other
RC_AA287138	AA287138	ESTs Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]	1.4	other
RC_AA287879	AA287879	ESTs Highly similar to GTP-BINDING PROTEIN SARA [Mus musculus]	1.4	?
RC_AA292128	AA292128	ESTs	1.4	other
RC_AA400093	AA400093	ESTs Weakly similar to HYPOTHETICAL 48.8 KD PROTEIN IN TRK2-MRS4 INTERGENIC REGION [Saccharomyces cerevisiae]	1.4	other
AA402937	AA402937	ESTs	1.4	other
RC_AA411882	AA411882	ESTs	1.4	other
RC_AA417895	AA417895	ESTs	1.4	SS,
AA422160	AA422160	H.sapiens NAP (nucleosome assembly protein) mRNA complete cds	1.4	other
RC_AA425100	AA425100	ESTs	1.4	other
RC_AA449068	AA449068	ESTs	1.4	TM
AA452724	AA452724	Homo sapiens TFAR19 mRNA complete cds	1.4	other
RC_AA460246	AA460246	ESTs Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]	1.4	other
RC_AA490949	AA490949	ESTs	1.4	other
RC_AA497015	AA497015	Homo sapiens chromosome 19 cosmid R32469	1.4	?
AB004884	AB004884	Homo sapiens mRNA for PKU-alpha partial cds	1.4	other
D38498_f	D38498	Human PMS5 mRNA (yeast mismatch repair gene PMS1 homologue) partial cds (C-terminal region)	1.4	?
RC_D80921_s	D80921	Homo sapiens clone 23965 mRNA sequence	1.4	other
RC_F04982	F04982	ESTs	1.4	other

FIGURE 7 (cont.)

RC_F09983	F09983	ESTs	1.4	other
H59417_s	H59417	ESTs	1.4	other
RC_H93708_s	H93708	CLEAVAGE SIGNAL-1 PROTEIN	1.4	other
L06419	L06419	Lysyl hydroxylase	1.4	SS,
M29580	M29580	Zinc finger protein 7 (KOX 4 clone HF.16)	1.4	other
M62810	M62810	Transcription factor 6-like 1 (mitochondrial transcription factor 1-like)	1.4	other
RC_N23972	N23972	ESTs	1.4	other
RC_N26722	N26722	ESTs	1.4	other
RC_N64244	N64244	ESTs	1.4	TM
RC_N66569	N66569	ESTs	1.4	?
RC_N92293	N92293	EST	1.4	?
RC_R01243	R01243	ESTs	1.4	other
RC_R09196	R09196	ESTs Moderately similar to M-phase phosphoprotein 11 [H.sapiens]	1.4	other
RC_R63925	R63925	ESTs	1.4	other
RC_R64660	R64660	ESTs	1.4	?
RC_T16226	T16226	ESTs	1.4	other
RC_T17440_f	T17440	ESTs	1.4	other
U07418	U07418	DNA mismatch repair protein MLH1	1.4	other
U12595	U12595	Human tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA partial cds	1.4	TM
U26727	U26727	Cyclin-dependent kinase inhibitor 2A (melanoma p16 inhibits CDK4)	1.4	other
U84720	U84720	Homo sapiens mRNA export protein (RAE1) mRNA complete cds	1.4	other
RC_W60473	W60473	ESTs	1.4	other
RC_W90146_f	W90146	ESTs	1.4	other
RC_W93379_s	W93379	H.sapiens nek2 mRNA for protein kinase	1.4	other
RC_Z38501	Z38501	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58]	1.4	other
RC_Z40041	Z40041	ESTs	1.3	other
RC_AA001386	AA001386	EST	1.3	other
RC_AA007234_s	AA007234	ESTs	1.3	other
RC_AA029264_s	AA029264	ESTs	1.3	other
RC_AA031357	AA031357	ESTs	1.3	other
RC_AA040696_s	AA040696	ESTs	1.3	other
RC_AA046619	AA046619	ESTs	1.3	other
RC_AA059051	AA059051	ESTs	1.3	other
AA059415	AA059415	ESTs Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]	1.3	other
AA083339	AA083339	ESTs	1.3	other
RC_AA098864	AA098864	ESTs	1.3	other
RC_AA101601	AA101601	ESTs Highly similar to Polio virus receptor protein [H.sapiens]	1.3	other
RC_AA122394	AA122394	ESTs	1.3	other
RC_AA126426_s	AA126426	Human brain secretory protein hSec10p (HSEC10) mRNA complete cds	1.3	other
RC_AA132007_f	AA132007	Down-regulator of transcription 1 TBP-binding (negative cofactor 2)	1.3	other
AA156670_s	AA156670	Homo sapiens agrin precursor mRNA partial cds	1.3	SS,
RC_AA206800	AA206800	ESTs Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]	1.3	TM
AA234817	AA234817	ESTs	1.3	other
RC_AA236200	AA236200	ESTs	1.3	other
RC_AA252079	AA252079	Homo sapiens mRNA for dachshund protein	1.3	other
RC_AA258189	AA258189	ESTs	1.3	other
RC_AA262889_s	AA262889	ESTs	1.3	other
RC_AA278650	AA278650	ESTs	1.3	other
AA329211_s	AA329211	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA complete cds	1.3	other
RC_AA338760	AA338760	ESTs	1.3	?
RC_AA398243	AA398243	ESTs Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]	1.3	other
RC_AA400195	AA400195	ESTs	1.3	other
RC_AA417569_i	AA417569	ESTs	1.3	TM
RC_AA428992	AA428992	ESTs	1.3	other
RC_AA435536	AA435536	ESTs	1.3	other
RC_AA443294	AA443294	Homo sapiens putative transcriptional repressor E2F-6 mRNA partial cds	1.3	other
RC_AA449071	AA449071	ESTs	1.3	TM
AA458542	AA458542	Homo sapiens chromosome 19 cosmid R32469	1.3	other
RC_AA461169	AA461169	ESTs	1.3	other
RC_AA464428	AA464428	ESTs	1.3	other
RC_AA465093	AA465093	ESTs	1.3	other
RC_AA485424	AA485424	ESTs	1.3	other
RC_AA487492_s	AA487492	Homo sapiens clone 23592 mRNA sequence	1.3	other

FIGURE 7 (cont.)

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RC_AA504499	AA504499	ESTs Highly similar to probable chloride channel 3 [H.sapiens]	1.3	other
RC_AA521471	AA521471	ESTs	1.3	other
RC_AA598506_s	AA598506	Human mRNA for KIAA0179 gene partial cds	1.3	other
RC_AA598675	AA598675	ESTs	1.3	other
RC_AA599718	AA599718	H.sapiens mRNA for translin associated protein X	1.3	other
RC_D11718	D11718	ESTs	1.3	?
D87466	D87466	Human mRNA for KIAA0276 gene partial cds	1.3	other
RC_F13663	F13663	ESTs	1.3	other
RC_H26417	H26417	ESTs	1.3	other
RC_H38086	H38086	Human N-ethylmaleimide-sensitive factor mRNA partial cds	1.3	other
RC_H38828_s	H38828	H.sapiens RBQ-1 mRNA	1.3	other
RC_H60061	H60061	ESTs Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]	1.3	other
RC_H71863_s	H71863	Zinc finger protein 139 (clone pHZ-37)	1.3	other
RC_H83438_s	H83438	Homo sapiens mRNA for DDS1beta protein complete cds	1.3	other
M64929	M64929	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform	1.3	other
M95767	M95767	DI-N-ACETYLCHITOBIASE PRECURSOR	1.3	SS,
RC_N20630_i	N20630	ESTs	1.3	other
RC_N24732	N24732	ESTs	1.3	other
RC_N51855	N51855	ESTs Moderately similar to NAD(+) ADP-RIBOSYLTRANSFERASE [D.melanogaster]	1.3	other
RC_R49886	R49886	ESTs	1.3	SS,
RC_T23932_f	T23932	ESTs	1.3	other
RC_T40707	T40707	ESTs	1.3	other
RC_T59859	T59859	ESTs	1.3	other
RC_T64438	T64438	ESTs Weakly similar to C01A2.4 [C.elegans]	1.3	TM
T68510	T68510	ESTs	1.3	other
RC_T95591	T95591	ESTs	1.3	other
U02680	U02680	Human protein tyrosine kinase mRNA complete cds	1.3	other
U28686	U28686	Human putative RNA binding protein RNPL mRNA complete cds	1.3	other
U66561	U66561	Human kruppel-related zinc finger protein (ZNF184) mRNA partial cds	1.3	other
U96113	U96113	EST - U96113	1.3	other
RC_W52065_f	W52065	Homo sapiens mRNA for KIAA0539 protein complete cds	1.3	?
RC_W67524	W67524	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence	1.3	TM
RC_W86978	W86978	ESTs	1.3	other
X69398	X69398	CD47 antigen (Rh-related antigen integrin-associated signal transducer)	1.3	SS,TM
X97544	X97544	H.sapiens mRNA for TIM17 preprotein translocase	1.3	TM
RC_Z41963_r	Z41963	Homo sapiens HP protein (HP) mRNA complete cds	1.3	?
Z46629	Z46629	SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversal)	1.3	other
RC_AA010188	AA010188	ESTs	1.2	other
RC_AA025746	AA025746	ESTs	1.2	other
AA112222	AA112222	EST - AA112222	1.2	other
AA147543	AA147543	ESTs	1.2	SS,
AA355201	AA355201	ESTs	1.2	SS,TM
RC_AA398222	AA398222	ESTs	1.2	other
RC_AA411708	AA411708	Homo sapiens clone 23685 mRNA sequence	1.2	other
RC_AA433943	AA433943	ESTs Highly similar to 50S RIBOSOMAL PROTEIN L13 [Mycobacterium leprae]	1.2	other
RC_AA464758	AA464758	ESTs	1.2	other
RC_H05635	H05635	ESTs	1.2	TM
L38961	L38961	Integral transmembrane protein 1	1.2	TM
N42440	N42440	ESTs Weakly similar to hnRNA-binding protein M4 [H.sapiens]	1.2	other
RC_N55304_s	N55304	ESTs	1.2	other
RC_N67104	N67104	ESTs	1.2	other
RC_N68622	N68622	ESTs Highly similar to HYPOTHETICAL 27.5 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION [Saccharomyces cerevisiae]	1.2	other
RC_N71027	N71027	ESTs	1.2	other
RC_N74635	N74635	ESTs	1.2	other
RC_R62444	R62444	ESTs	1.2	other
RC_T17498	T17498	ESTs	1.2	TM
RC_T32794_s	T32794	ESTs	1.2	other
RC_T85190	T85190	EST - RC_T85190	1.2	?
RC_T99364	T99364	ESTs Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	1.2	other
U20240	U20240	CCAAT/enhancer binding protein (C/EBP) gamma	1.2	other
U51698	U51698	ESTs	1.2	?
U79718	U79718	Human endonuclease III homolog mRNA complete cds	1.2	other
W03007	W03007	ESTs	1.2	other

FIGURE 7 (cont.)

RC_W61011	W61011	ESTs	1.2	other
RC_W87544	W87544	ESTs	1.2	other
X02751	X02751	Neuroblastoma RAS viral (v-ras) oncogene homolog	1.2	?
Z14077_s	Z14077	YY1 transcription factor	1.2	other
RC_Z38839	Z38839	ESTs	1.2	?

FIGURE 7 (cont.)
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Title	Accession	PROBESET	[illegible]	[illegible]
fibronectin 1	T78889	RC_T78889_s	3.1	44.4
ESTs	AA393803	RC_AA393803	3.9	24.6
Human heart mRNA for heat shock protein 9; partial cds	H88540	RC_H88540	2.8	22.0
ESTs	W31478	RC_W31478_s	1.5	20.8
ESTs; Weakly similar to (defline not available 4454131) [D.melanogaster]	W79424	RC_W79424_s	1.8	19.7
Homo sapiens RGS-GAIP interacting protein GIPC mRNA; complete cds	AA149940	RC_AA149940	1.2	17.5
collagen; type I; alpha 2	J03464	J03464_s	8.7	17.3
Homo sapiens mRNA for actin-related protein; complete cds	W48638	RC_W48638	3.0	17.3
MYOSIN REGULATORY LIGHT CHAIN 2; NONSARCOMERIC	W92462	RC_W92462	1.1	16.1
ESTs; Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Ascaris suum]	D63079	D63079_s	1.9	15.9
ESTs	AA255874	RC_AA255874	1.7	15.8
fibronectin 1	X02761	X02761	3.6	15.2
TFAR19 novel apoptosis-related gene	R71082	RC_R71082_s	2.5	15.2
ESTs; Highly similar to FRIZZLED PROTEIN PRECURSOR [Drosophila melanogaster]	AA449749	RC_AA449749	10.6	14.7
ESTs	AA243721	RC_AA243721	1.5	14.0
Homo sapiens mRNA for KIAA886 protein; complete cds	AA600169	RC_AA600169	1.2	13.9
ESTs	AA182001	RC_AA182001_i	1.2	13.8
dihydropyrimidinase-like 2	T10322	RC_T10322	0.8	13.5
	M97935	AFFX-HUMISGF3A/M97935_3	2.3	13.5
ESTs	AA186897	RC_AA186897	4.5	13.5
lactate dehydrogenase B	T16206	RC_T16206_i	0.6	13.1
ESTs; Weakly similar to SAS [H.sapiens]	AA365742	AA365742_s	3.2	13.0
ESTs	AA621274	RC_AA621274_i	1.1	12.8
ESTs; Highly similar to GALECTIN-1 [Homo sapiens]	H25999	RC_H25999_s	2.5	12.7
H.sapiens gene from PAC 295C6; similar to rat PO44	AA281132	RC_AA281132	1.9	12.6
Human CCAAT-box-binding factor (CBF) mRNA; complete cds	T47491	RC_T47491	1.4	12.3
ESTs; Moderately similar to 25E8.I [D.melanogaster]	W79421	RC_W79421	1.2	12.0
ESTs; Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-25 KD [Bos taurus]	H78385	RC_H78385_s	1.7	11.7
ESTs	F13673	RC_F13673	14.8	11.5
desmoplakin (DPI; DPII)	AA247685	AA247685	4.3	11.5
immunoglobulin gamma 3 (Gm marker)	H64493	RC_H64493_f	1.6	11.4
Pantophysin [human; keratinocyte line HaCaT; mRNA; 216 nt]	R72029	RC_R72029_f	1.4	11.4
ESTs	D79891	D79891	2.7	11.4
ESTs	AA167393	RC_AA167393_s	2.0	11.3
Human transcriptional coactivator PC4 mRNA; complete cds	D57317	RC_D57317	1.9	11.2
ESTs	N67507	RC_N67507	1.3	11.2
neurotrophic tyrosine kinase; receptor-related 1	C15347	RC_C15347	1.2	11.2
ESTs; Highly similar to HYPOTHETICAL 1.4 KD PROTEIN IN UBP5-SPT15 INTERGENIC REGION [Saccharomyces cerevisiae]	AA027086	RC_AA027086	2.3	11.2
ESTs; Weakly similar to EBNA-2 NUCLEAR PROTEIN [Human herpesvirus 4 (strain b95-8)]	AA598781	RC_AA598781	4.0	11.2
Homo sapiens actin-related protein Arp2 (ARP2) mRNA; complete cds	C16379	C16379	1.5	11.1

FIGURE 8

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tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein; eta polypeptide	H69844	RC_H69844_s	1.5	11.1
Homo sapiens mRNA for DCRA; complete cds	R97540	RC_R97540_f	1.0	11.1
Homo sapiens chaperonin containing t-complex polypeptide 1; beta subunit (Cctb) mRNA; complete cds	AA488991	RC_AA488991_s	1.5	10.9
Homo sapiens actin-related protein Arp2 (ARP2) mRNA; complete cds	AF006082	AF006082	1.6	10.9
ESTs	T23457	RC_T23457	3.7	10.8
Human (clone E5.1) RNA-binding protein mRNA; complete cds	T33593	RC_T33593_s	2.0	10.8
Homo sapiens clone 24416 mRNA sequence	AA417761	RC_AA417761	1.4	10.7
ESTs	N39152	RC_N39152	1.5	10.7
ESTs	AA429539	AA429539_f	1.8	10.7
ESTs	T30617	T30617	1.1	10.6
small inducible cytokine A5 (RANTES)	AA486072	RC_AA486072_i	1.4	10.6
ESTs	R79392	RC_R79392	3.3	10.5
calumenin	AA477316	RC_AA477316	2.8	10.5
ESTs	R54421	RC_R54421_s	1.4	10.4
UDP-N-acteylglucosamine pyrophosphorylase 1; Sperm associated antigen 2	AA447549	RC_AA447549	1.9	10.3
Homo sapiens HRIHFB2115 mRNA; partial cds	H11320	RC_H11320_s	2.0	10.3
ESTs; Moderately similar to putative G-binding protein [H.sapiens]	H94877	RC_H94877	1.8	10.2
protein kinase; cAMP-dependent; catalytic; alpha	H89514	RC_H89514_s	1.0	10.2
ESTs	F10354	RC_F10354_f	1.0	10.1
ESTs	AA173981	RC_AA173981	1.2	10.0
zn13e4.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:547326 5' similar to gb:J2683 ADP,ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (HUMAN);, mRNA sequence	AA084874	AA084874_f	0.9	10.0
ESTs; Highly similar to YME1 PROTEIN [Saccharomyces cerevisiae]	AA452161	RC_AA452161	1.8	9.9
ESTs	N93521	RC_N93521	1.5	9.9
small inducible cytokine A5 (RANTES)	M21121	M21121_s	0.9	9.9
ESTs	AA490112	RC_AA490112_s	2.1	9.9
ESTs; Highly similar to HYPOTHETICAL 16.3 KD PROTEIN IN DUR1;2-NGR1 INTERGENIC REGION [Saccharomyces cerevisiae]	AA053139	RC_AA053139	3.2	9.7
ESTs	AA446461	RC_AA446461	1.1	9.7
C-terminal binding protein 2	N50048	RC_N50048	2.1	9.7
Homo sapiens mRNA for putative progesterone binding protein	N66130	RC_N66130	1.4	9.6
ESTs	AA490341	RC_AA490341_s	1.4	9.5
transcription factor AP-2 alpha (activating enhancer-binding protein 2 alpha)	R38044	RC_R38044_f	9.4	9.4
ESTs; Highly similar to (defline not available 468665) [H.sapiens]	W73805	W73805	1.2	9.4
cathepsin B	AA608751	RC_AA608751_i	2.1	9.3
ESTs; Highly similar to heat shock factor binding protein 1 HSBP1 [H.sapiens]	D59525	RC_D59525_f	1.8	9.3
ESTs	AA280409	RC_AA280409_s	2.1	9.3
ESTs; Weakly similar to similar to yeast adenylate cyclase [H.sapiens]	N77542	N77542	1.6	9.2
ESTs	D60296	RC_D60296	1.7	9.2
ESTs; Weakly similar to VACUOLAR ATP SYNTHASE 54 KD SUBUNIT [Saccharomyces cerevisiae]	Z39349	RC_Z39349	1.6	9.2
solute carrier family 12 (sodium/potassium/chloride transporters); member 2	AA262080	RC_AA262080	1.4	9.2
iduronate 2-sulfatase (Hunter syndrome)	H14810	RC_H14810_s	1.0	9.1

FIGURE 8
(Cont.)

ESTs	T90531	RC_T90531	1.5	9.1
ESTs	Z40959	RC_Z40959_f	1.0	8.9
collagen-binding protein 2 (colligen 2)	H27188	RC_H27188_f	2.6	8.9
HMT1 (hnRNP methyltransferase; S. cerevisiae)-like 1	T81393	RC_T81393_s	1.8	8.8
Homo sapiens lysophospholipase (LPL1) mRNA; complete cds	AA252436	AA252436	1.6	8.8
Homo sapiens TACC1 (TACC1) mRNA; complete cds	N46837	RC_N46837	2.4	8.7
ESTs	AA122386	RC_AA122386	6.6	8.7
ESTs; Highly similar to LEUCYL-TRNA SYNTHETASE; CYTOPLASMIC [Saccharomyces cerevisiae]	R32993	R32993_s	1.6	8.6
NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 6 (17kD; B17)	C16329	C16329	0.9	8.6
ESTs; Weakly similar to transporter protein [H.sapiens]	R80048	R80048	1.2	8.5
ESTs	AA102644	RC_AA102644	1.8	8.5
ESTs; Weakly similar to (defline not available 4234) [D.melanogaster]	AA393805	RC_AA393805	1.1	8.4
ESTs; Weakly similar to putative Rab5-interacting protein (clone L1-94) [H.sapiens]	H68794	RC_H68794	1.5	8.4
ESTs	AA399445	RC_AA399445	0.9	8.4
Homo sapiens Arp2/3 protein complex subunit p16-Arc (ARC16) mRNA; complete cds	AF006088	AF006088	1.5	8.3
ESTs	AA278329	RC_AA278329_f	3.1	8.3
ESTs	AA187490	RC_AA187490	3.6	8.3
ESTs	N90933	RC_N90933	1.0	8.2
ESTs; Weakly similar to predicted using Genefinder [C.elegans]	D31058	D31058_s	2.1	8.2
immumoglobulin lambda gene cluster	T67053	RC_T67053_f	1.2	8.2
epithelial membrane protein 2	T88721	RC_T88721_s	1.3	8.2
Homo sapiens actin-related protein Arp3 (ARP3) mRNA; complete cds	AF006083	AF006083	1.8	8.1
ESTs	AA040923	RC_AA040923	1.8	8.1
INTERFERON-ALPHA INDUCED 11.5 KD PROTEIN	AA161292	RC_AA161292_s	1.5	8.0
ESTs	W85875	RC_W85875	0.9	8.0
Human mRNA for KIAA336 gene; complete cds	AA608903	RC_AA608903	1.4	7.9
ESTs; Moderately similar to KIAA438 [H.sapiens]	H81379	RC_H81379_s	1.3	7.9
H. sapiens cDNA for RFG	AA194075	RC_AA194075_f	0.4	7.9
ESTs; Weakly similar to cDNA EST EMBL:T1157 comes from this gene [C.elegans]	N67312	RC_N67312	1.7	7.9
	M10098	AFFX-HUMRGE/M10098_5	1.1	7.9
Fibronectin, Alt. Splice 1	HG3044-HT3742	HG3044-HT3742	3.0	7.8
cytochrome c oxidase subunit VII-related protein	AA025213	RC_AA025213	1.3	7.8
CD74 antigen (invariant polypeptide of major histocompatibility complex; class II antigen-associated)	W67577	RC_W67577_s	1.2	7.8
ESTs; Weakly similar to neural differentiation-associated protein [M.musculus]	AA233342	RC_AA233342	3.8	7.7
ESTs	AA291159	RC_AA291159_f	0.7	7.7
ESTs	N63604	RC_N63604	3.6	7.7
HEAT SHOCK 7 KD PROTEIN 1	T66307	RC_T66307_f	1.3	7.6
Human DNA sequence from clone 3M3 on chromosome 6p22.1-22.3. Contains three novel genes; one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant; worm; yeast and archaea bacterial genes; and the first exon of the KIAA319 gene. Contains E	AA243497	RC_AA243497	1.7	7.6
Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT)	AA600134	RC_AA600134	1.7	7.6
ESTs	H61476	RC_H61476_s	1.6	7.6
transforming growth factor; beta receptor II (7-8kD)	H90886	RC_H90886_s	0.8	7.6

FIGURE 8
(Cont.)

ESTs; Weakly similar to ubiquitous TPR motif; Y isoform [H.sapiens]	AA449320	RC_AA449320	1.0	7.5
ESTs; Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III [Caenorhabditis elegans]	N48787	RC_N48787	1.9	7.5
Homo sapiens heterogeneous nuclear ribonucleoprotein R mRNA; complete cds	C16574	C16574	1.7	7.5
Homo sapiens mRNA for CMP-sialic acid transporter; complete cds	AA481542	RC_AA481542_s	1.2	7.5
ESTs; Weakly similar to F15D4.3 [C.elegans]	N89563	N89563_s	2.0	7.5
ESTs	AA490262	RC_AA490262	2.9	7.5
ESTs; Weakly similar to similar to Yeast hypothetical protein L8167.12 like [C.elegans]	AA621349	RC_AA621349	1.3	7.5
ESTs; Highly similar to (defline not available 412715) [H.sapiens]	C01782	C01782	1.9	7.4
ESTs	AA402492	RC_AA402492	1.7	7.4
	AFFX-M27830	AFFX-M27830_5	0.5	7.4
ESTs; Weakly similar to C17H11.6 [C.elegans]	AA194237	RC_AA194237	1.7	7.4
ESTs	H10933	RC_H10933	4.6	7.4
Human spliceosomal protein (SAP 49) gene; complete cds	AA463934	RC_AA463934	1.6	7.3
Human mRNA for KIAA174 gene; complete cds	R16097	RC_R16097_s	1.2	7.2
ESTs	AA128486	RC_AA128486	1.5	7.2
ESTs; Weakly similar to HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION [Saccharomyces cerevisiae]	R59694	RC_R59694_s	1.4	7.1
ESTs	AA428090	AA428090	7.0	7.0
ESTs	H88486	RC_H88486_f	1.5	7.0
ESTs; Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT [Canis familiaris; Mus musculus]	D79052	D79052_s	3.1	7.0
C-terminal binding protein 2	AA417287	RC_AA417287	2.6	7.0
protein kinase; mitogen-activated 6 (extracellular signal-regulated kinase; p97)	T32837	RC_T32837_s	1.1	6.9
tumor rejection antigen (gp96) 1	D51235	RC_D51235_f	1.2	6.9
ESTs; Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]	F04258	RC_F04258_s	3.3	6.9
Human mRNA for KIAA35 gene; partial cds	D51272	RC_D51272_s	3.2	6.9
Homo sapiens mRNA from chromosome 5q31-33 region	T99196	RC_T99196_s	1.4	6.9
H.sapiens mRNA for serine palmitoyltransferase; subunit I	T39740	T39740_s	1.3	6.9
Homo sapiens calcium binding protein (ALG-2) mRNA; complete cds	AA122332	RC_AA122332	1.7	6.9
ESTs	T92245	RC_T92245_i	0.9	6.9
ESTs	F01813	RC_F01813_s	3.1	6.9
ESTs; Highly similar to putative Rab5-interacting protein {clone L1-57} [H.sapiens]	AA292533	RC_AA292533	1.3	6.9
ESTs; Moderately similar to POSSIBLE DNA-REPAIR PROTEIN XP-E [Cercopithecus aethiops]	AA287961	RC_AA287961	1.6	6.8
ESTs	AA053883	RC_AA053883	0.7	6.8
peptidylprolyl isomerase B (cyclophilin B)	H96665	RC_H96665_s	2.2	6.8
connective tissue growth factor	AA449789	RC_AA449789_f	1.9	6.8
Homo sapiens exportin t mRNA; complete cds	H99877	RC_H99877	4.0	6.8
ESTs; Weakly similar to Ydr372cp [S.cerevisiae]	AA191014	RC_AA191014	1.7	6.8
ESTs; Highly similar to (defline not available 4426962) [H.sapiens]	H82061	RC_H82061	1.2	6.8
ESTs	AA433947	RC_AA433947	1.8	6.8
ESTs	AA236280	RC_AA236280	1.5	6.8
ESTs; Highly similar to DTDP-4-DEHYDRORHAMNOSE REDUCTASE [Salmonella typhimurium]	AA521303	RC_AA521303	0.8	6.7
N-acetylglucosaminyl transferase component Gpi1	W94289	RC_W94289	1.1	6.7

FIGURE 8
(Cont.)

proteasome (prosome; macropain) 26S subunit; non-ATPase; 1	AA460532	RC_AA460532	1.5	6.6
ESTs	AA398197	RC_AA398197	1.9	6.6
cytochrome c oxidase subunit IV	AA236361	RC_AA236361	1.2	6.6
Thymosin; beta 1	T59161	RC_T59161_s	2.6	6.6
Homo sapiens mRNA for KIAA733 protein; partial cds	H88033	H88033_s	1.2	6.6
ESTs	H86543	RC_H86543_f	1.8	6.6
glucan (1;4-alpha-); branching enzyme 1 (glycogen branching enzyme; Andersen disease; glycogen storage disease type IV)	H71861	RC_H71861_s	0.9	6.6
ESTs	T95333	RC_T95333	5.3	6.6
ESTs; Moderately similar to !!!! ALU CLASS C WARNING ENTRY !!!! [H.sapiens]	AA425447	RC_AA425447	1.7	6.6
Homo sapiens GA17 protein mRNA; complete cds	AA147725	RC_AA147725	2.5	6.5
lactate dehydrogenase A	AA112012	RC_AA112012_s	2.0	6.5
ESTs	AA621159	RC_AA621159	1.8	6.5
ESTs; Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]	AA429228	AA429228	1.6	6.5
collagen; type I; alpha 2	Z74616	Z74616	9.9	6.5
ESTs; Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	AA608668	RC_AA608668	1.0	6.5
ESTs	N93155	RC_N93155_i	1.8	6.5
ESTs	D51401	RC_D51401_s	1.4	6.3
Homo sapiens mRNA for KIAA96 protein; partial cds	AA250870	AA250870_s	2.3	6.3
ESTs	AA429636	RC_AA429636	0.9	6.3
ESTs; Weakly similar to similar to Yeast hypothetical protein L8167.12 like [C.elegans]	H73484	RC_H73484_s	1.3	6.3
ESTs	AA489091	RC_AA489091	1.4	6.3
ESTs; Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION [Saccharomyces cerevisiae]	H84891	RC_H84891_i	1.1	6.3
ESTs	AA001049	RC_AA001049	1.1	6.3
ESTs; Weakly similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]	N20066	RC_N20066	1.2	6.2
ESTs; Highly similar to RAS-RELATED PROTEIN RAB-1 [Canis familiaris]	AA428870	RC_AA428870	1.8	6.2
ESTs	W16836	RC_W16836_s	2.2	6.2
ESTs	H07873	RC_H07873	1.2	6.2
ESTs	W58619	RC_W58619	1.7	6.2
Homo sapiens mRNA for KIAA737 protein; complete cds	N66219	RC_N66219	1.3	6.2
bone morphogenetic protein 6	AA092596	AA092596	1.1	6.2
Homo sapiens DNA from chromosome 19-cosmid R3879 containing USF2; genomic sequence	R36881	RC_R36881_s	1.5	6.2
ESTs	AA179387	RC_AA179387	4.0	6.1
ESTs; Moderately similar to fibronectin [H.sapiens]	AA279397	RC_AA279397	1.3	6.1
ESTs; Highly similar to MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE [Xenopus laevis]	T96374	RC_T96374	0.8	6.1
ESTs	AA465194	RC_AA465194	1.7	6.1
Human amino acid transport-related protein mRNA; complete cds	AA152418	RC_AA152418	1.1	6.1
ESTs	AA447971	RC_AA447971	5.1	6.1
ESTs	W38419	RC_W38419_f	0.9	6.1
pigment epithelium-derived factor	AA111889	RC_AA111889	1.5	6.1
ESTs	W42508	RC_W42508	1.1	6.1
ESTs	N91023	RC_N91023	3.3	6.1
membrane fatty acid (lipid) desaturase	AA186666	RC_AA186666	2.4	6.0

FIGURE 8
(Cont.)

collagen; type I; alpha 2	H88674	RC_H88674_s	3.0	6.0
Homo sapiens 3-phosphoglycerate dehydrogenase mRNA; complete cds	T83646	RC_T83646	0.9	6.0
HMT1 (hnRNP methyltransferase; S. cerevisiae)-like 2	W46810	RC_W46810_s	3.2	5.9
LYMPHOCYTE-SPECIFIC PROTEIN LSP1	T49291	RC_T49291_s	1.0	5.9
Homo sapiens secreted cement gland protein XAG-2 homolog (hAG-2/R) mRNA; complete cds	AA421562	RC_AA421562	1.3	5.9
Homo sapiens clone 23956 mRNA; partial cds	W69452	RC_W69452	1.1	5.9
ESTs; Moderately similar to Similar to S.cerevisiae hypothetical protein L3111 [H.sapiens]	N79531	RC_N79531_s	3.1	5.9
ESTs	AA406163	RC_AA406163	1.1	5.9
ESTs	AA454157	RC_AA454157	1.2	5.9
Homo sapiens clone 2394 mRNA sequence	AA609773	RC_AA609773	5.5	5.9
ESTs	AA156897	AA156897_s	3.7	5.8
Homo sapiens insulin induced protein 1 (INSIG1) gene; complete cds	AA021623	RC_AA021623_s	1.1	5.8
biliverdin reductase A	D51072	RC_D51072_s	1.8	5.8
ESTs; Weakly similar to hypothetical protein [H.sapiens]	T97257	RC_T97257_f	1.4	5.8
quinoid dihydropteridine reductase	T69009	RC_T69009_s	0.5	5.8
ESTs	AA489459	RC_AA489459	1.1	5.7
ESTs; Highly similar to follistatin-related protein [H.sapiens]	D51110	RC_D51110_s	2.1	5.7
ESTs	AA452855	RC_AA452855	2.0	5.7
ESTs; Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]	AA442125	RC_AA442125	1.3	5.7
cell division cycle 42 (GTP-binding protein; 25kD)	N63172	RC_N63172	2.1	5.7
ESTs; Highly similar to EUKARYOTIC INITIATION FACTOR 4 GAMMA [Oryctolagus cuniculus]	W84870	RC_W84870_s	1.2	5.7
ESTs	AA121121	RC_AA121121	1.3	5.7
ESTs; Moderately similar to HN1 [M.musculus]	AA436027	RC_AA436027	1.9	5.7
ESTs	AA441923	RC_AA441923	5.6	5.7
ESTs; Weakly similar to brain-specific L-proline transporter	AA460049	AA460049_s	1.2	5.7
ESTs	AA181911	RC_AA181911	0.7	5.6
ESTs	AA053962	RC_AA053962	1.2	5.6
ESTs	AA453783	RC_AA453783_s	3.7	5.6
ESTs	N32811	RC_N32811	1.8	5.6
Human transposon-like element mRNA	M23161	M23161	0.8	5.6
ESTs	AA485655	RC_AA485655	2.3	5.6
ESTs; Weakly similar to (defline not available 446577) [H.sapiens]	Z41803	RC_Z41803	1.1	5.6
Homo sapiens short form transcription factor C-MAF (c-maf) mRNA; complete cds	AA496914	RC_AA496914	0.8	5.6
glioblastoma amplified sequence	AA095021	AA095021	1.0	5.6
karyopherin alpha 1 (importin alpha 5)	N35247	RC_N35247	1.2	5.6
Human mRNA for KIAA69 gene; partial cds	AA148318	RC_AA148318_s	2.3	5.6
Homo sapiens clone 23675 mRNA sequence	Z39978	RC_Z39978	1.1	5.6
ESTs	H73161	RC_H73161_f	1.2	5.6
Homo sapiens clone 23585 mRNA sequence	AA453461	RC_AA453461	1.6	5.5
ESTs	H98153	RC_H98153	7.0	5.5
desmoplakin (DPI; DPII)	H90899	RC_H90899	5.4	5.5
sterol regulatory element binding transcription factor 2	AA053886	RC_AA053886_s	1.2	5.5
ESTs; Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]	AA134138	RC_AA134138	1.4	5.5

FIGURE 8
(Cont.)

ESTs; Highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus musculus]	AA082057	RC_AA082057	1.1	5.5
ESTs; Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMI4-PAC2 INTERGENIC REGION (Saccharomyces cerevisiae]	AA609710	RC_AA609710	5.5	5.5
heterogeneous nuclear ribonucleoprotein A1	AA416785	RC_AA416785_f	2.2	5.5
Human Chromosome 16 BAC clone CIT987SK-A-362G6	U95740	U95740_rna1	0.9	5.5
Homo sapiens Arp2/3 protein complex subunit p21-Arc (ARC21) mRNA; complete cds	AF006086	AF006086	1.4	5.4
ESTs	AA478387	RC_AA478387	1.0	5.4
Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA; complete cds	AA455970	RC_AA455970	1.8	5.4
ESTs; Weakly similar to NIPSNAP2 protein [H.sapiens]	R49052	RC_R49052	1.3	5.4
ESTs	AA235803	RC_AA235803_i	2.5	5.4
ESTs	T15482	RC_T15482_f	0.7	5.4
NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 3 (12kD; B12)	AA040759	RC_AA040759_s	1.0	5.4
Human mRNA for KIAA263 gene; complete cds	T16989	RC_T16989_f	1.2	5.4
ESTs	R27975	RC_R27975	1.2	5.4
ESTs; Moderately similar to (defline not available 445515) [H.sapiens]	AA047187	RC_AA047187	0.8	5.4
ESTs	W45417	RC_W45417	1.0	5.4
ESTs; Weakly similar to zinc finger protein [H.sapiens]	AA487297	RC_AA487297	1.6	5.4
	M27830	AFFX-M27830_5	0.6	5.4
ESTs	AA258614	RC_AA258614_s	2.0	5.3
ESTs; Weakly similar to cDNA EST EMBL:T1157 comes from this gene [C.elegans]	AA313414	AA313414_s	1.5	5.3
secreted frizzled-related protein 4	AA291725	RC_AA291725	5.3	5.3
ESTs	AA282179	RC_AA282179	0.9	5.3
Human pim-2 protooncogene homolog pim-2h mRNA; complete cds	AA227480	RC_AA227480_s	0.8	5.3
ESTs; Weakly similar to ORF YOR126c [S.cerevisiae]	AA249311	AA249311	1.4	5.3
ESTs	W36290	W36290_s	1.7	5.3
Homo sapiens hJTB mRNA; complete cds	AA071387	AA071387	1.7	5.3
Homo sapiens mRNA for putative vacuolar proton ATPase membrane sector associated protein M8-9	D51241	RC_D51241_s	2.2	5.3
ESTs	T92735	RC_T92735	1.7	5.3
splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated)	T64923	RC_T64923_f	1.2	5.3
ESTs	W20404	RC_W20404_s	1.1	5.2
high-mobility group (nonhistone chromosomal) protein 1	AA486201	RC_AA486201_s	1.1	5.2
ESTs	T15386	RC_T15386	0.9	5.2
ESTs	AA608657	RC_AA608657_f	2.1	5.2
ESTs	AA236276	RC_AA236276	1.4	5.2
ESTs; Weakly similar to cDNA EST EMBL:T1585 comes from this gene [C.elegans]	AA598439	RC_AA598439	1.4	5.2
ubiquitin-specific protease 1	D62657	RC_D62657	0.5	5.2
ESTs	AA419507	AA419507	1.0	5.2
ESTs	AA496962	RC_AA496962	0.9	5.2
Homo sapiens clone 23596 mRNA sequence	AA425741	RC_AA425741	0.7	5.2
Homo sapiens clone 23714 mRNA sequence	AA147364	RC_AA147364	0.9	5.2
ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	Z21420	Z21420	1.3	5.2

FIGURE 8
(Cont.)

ESTs	T15434	RC_T15434_s	0.9	5.1
ESTs	W95416	RC_W95416	1.1	5.1
Homo sapiens clone 23675 mRNA sequence	AA018804	AA018804	2.9	5.1
Homo sapiens mRNA for KIAA447 protein; complete cds	C02016	C02016	1.4	5.1
apolipoprotein H (beta-2-glycoprotein I)	T83356	RC_T83356_s	0.3	5.1
ESTs; Moderately similar to weak similarity to Arabidopsis thaliana ubiquitin-like protein 8 [C.elegans]	D31544	D31544_s	3.2	5.1
Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA; complete cds	AF010193	AF010193	1.0	5.1
ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	AA155779	RC_AA155779	1.7	5.1
ESTs; Highly similar to 6S RIBOSOMAL PROTEIN L26 [Homo sapiens; Mus musculus]	D80128	RC_D80128_f	1.6	5.1
ESTs	AA018907	RC_AA018907_s	2.0	5.1
immunoglobulin gamma 3 (Gm marker)	J00231	J00231_f	1.4	5.1
ESTs	N81162	N81162	2.0	5.1
ESTs	AA599850	RC_AA599850	1.3	5.1
ESTs	AA460935	RC_AA460935	1.8	5.0
ESTs; Highly similar to heat shock factor binding protein 1 HSBP1 [H.sapiens]	AA490864	RC_AA490864	1.4	5.0
ESTs	W80516	W80516	1.0	5.0
ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	AA046939	RC_AA046939_s	1.2	5.0
Human DNA sequence from clone 149A16 on chromosome 22q12-13. Contains an IGLC (Immunoglobulin Lambda Chain C) pseudogene; the RFPL3 and RFPL3S genes for Ret finger protein-like 3 and Ret finger protein-like 3 antisense respectively; a gene for a novel Imm	AA151882	RC_AA151882	1.4	5.0
ESTs	T72867	RC_T72867	1.2	5.0
myosin VI	AB002387	AB002387	4.5	5.0
GM2 ganglioside activator protein	AA167512	RC_AA167512	1.3	5.0
ESTs; Moderately similar to putative p15 [H.sapiens]	AA481060	RC_AA481060	1.3	5.0
ESTs	N69086	RC_N69086	1.5	5.0
ESTs; Highly similar to heat shock factor binding protein 1 HSBP1 [H.sapiens]	C14243	RC_C14243_f	1.7	5.0
neuroblastoma RAS viral (v-ras) oncogene homolog	AA431977	RC_AA431977	1.4	5.0
Homo sapiens mRNA for putative vacuolar proton ATPase membrane sector associated protein M8-9	R25326	R25326	0.9	5.0
butyrate response factor 1 (EGF-response factor 1)	H40424	RC_H40424_s	1.4	5.0
H factor (complement)-like 1	AA235873	RC_AA235873_s	0.6	5.0
ESTs; Weakly similar to predicted using Genefinder [C.elegans]	AA252040	RC_AA252040	1.5	5.0
ESTs	R62589	RC_R62589_f	1.2	5.0
Human mRNA for KIAA171 gene; complete cds	AA028889	RC_AA028889_s	1.1	5.0
ESTs; Highly similar to G protein-coupled receptor kinase 6; splice variant B [H.sapiens]	AA040699	RC_AA040699	1.0	4.9
ESTs; Highly similar to (defline not available 45813) [H.sapiens]	AA488414	RC_AA488414	1.2	4.9
CYTOCHROME C	M22877	M22877	0.8	4.9
ESTs; Highly similar to synapsin I [R.norvegicus]	T15663	RC_T15663_s	0.8	4.9
lysozyme (renal amyloidosis)	J03801	J03801_f	0.9	4.9
ESTs	W88642	RC_W88642	1.0	4.9
ESTs	W57813	RC_W57813_i	0.8	4.9
ESTs	AA046405	RC_AA046405	1.6	4.9
Homo sapiens metalloprotease 1 (MP1) mRNA; complete cds	AA132969	RC_AA132969_s	2.0	4.9

FIGURE 8
(Cont.)

Homo sapiens mRNA for KIAA829 protein; partial cds	H01766	H01766_s	1.3	4.9
ESTs; Weakly similar to synapse associated protein sap47-2 [D.melanogaster]	N51752	RC_N51752	2.5	4.9
secreted phosphoprotein 1 (osteopontin; bone sialoprotein I; early T-lymphocyte activation 1)	U20758	U20758_rna1	1.9	4.9
ESTs	AA283085	RC_AA283085_s	0.6	4.9
ATPase; Ca++ transporting; cardiac muscle; slow twitch 2	M23114	M23114	2.0	4.9
Deleted in oral cancer-1	AA600140	RC_AA600140	2.4	4.9
ESTs	W88755	RC_W88755	1.3	4.8
synuclein; alpha (non A4 component of amyloid precursor)	C13990	RC_C13990_f	0.6	4.8
ESTs; Weakly similar to KIAA638 protein [H.sapiens]	R73982	R73982	0.7	4.8
ESTs	AA281949	RC_AA281949	1.3	4.8
ESTs	AA134767	RC_AA134767_s	1.5	4.8
ESTs	AA453593	RC_AA453593_s	0.9	4.8
frizzled (Drosophila) homolog 1	AA358618	RC_AA358618_s	2.4	4.8
ESTs	H93552	RC_H93552	0.9	4.8
cyclin G2	D53233	RC_D53233	2.7	4.8
peptidylprolyl isomerase B (cyclophilin B)	H15847	RC_H15847_s	1.8	4.8
ESTs; Highly similar to (defline not available 439889) [H.sapiens]	AA256210	RC_AA256210	2.0	4.8
Homo sapiens clone 23698 mRNA sequence	R32440	RC_R32440	0.5	4.8
ESTs	C15078	RC_C15078_i	0.8	4.8
ESTs; Weakly similar to CH-TOG PROTEIN [H.sapiens]	AA486092	RC_AA486092	2.8	4.8
ESTs	C00038	C00038_s	2.8	4.8
ESTs	AA450281	RC_AA450281	1.0	4.8
Homo sapiens mRNA for KIAA663 protein; complete cds	N57577	RC_N57577	1.1	4.8
ferritin; light polypeptide	T73572	RC_T73572_f	1.1	4.8
ESTs; Highly similar to 5'-AMP-ACTIVATED PROTEIN KINASE; GAMMA-1 SUBUNIT [Rattus norvegicus]	AA114970	RC_AA114970_i	1.3	4.8
ESTs; Highly similar to ZYXIN [Gallus gallus]	H25769	RC_H25769_s	1.2	4.8
tubulin-specific chaperone a	AA504095	AA504095	1.6	4.8
ESTs	N25576	RC_N25576	1.1	4.8
Homo sapiens inner mitochondrial membrane translocase Tim23 (TIM23) mRNA; nuclear gene encoding mitochondrial protein; complete cds	AA442768	RC_AA442768_i	1.9	4.8
ESTs	AA235289	RC_AA235289	2.4	4.8
ESTs	N27198	RC_N27198	2.5	4.8
ESTs	AA479132	AA479132	1.7	4.8
ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	AA450228	RC_AA450228	1.5	4.7
calmodulin 1 (phosphorylase kinase; delta)	AA085590	RC_AA085590_s	1.3	4.7
Homo sapiens actin-related protein Arp3 (ARP3) mRNA; complete cds	AA199588	RC_AA199588	1.8	4.7
Human TAR DNA-binding protein-43 mRNA; complete cds	H16390	RC_H16390_s	1.3	4.7
Human TAR RNA loop binding protein (TRP-185) mRNA; complete cds	N70678	RC_N70678_s	1.5	4.7
Human transformer-2 alpha (htra-2 alpha) mRNA; complete cds	AA455812	AA455812	1.3	4.7
ESTs	AA057287	AA057287	0.7	4.7
ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	AA070801	RC_AA070801	6.3	4.7
ESTs; Highly similar to COMPLEMENT C1Q SUBCOMPONENT; A CHAIN PRECURSOR [Homo sapiens]	W87494	RC_W87494	1.2	4.7

FIGURE 8
(Cont.)

ESTs	AA490264	RC_AA490264	0.8	4.7
TAP binding protein (tapasin)	AA303745	AA303745_s	1.8	4.7
UDP-glucose dehydrogenase	AA454086	RC_AA454086_f	1.3	4.7
protein tyrosine phosphatase; receptor type; c polypeptide	Y00062	Y00062	0.6	4.6
ESTs	AA449333	RC_AA449333	2.9	4.6
ESTs; Highly similar to TURNED ON AFTER DIVISION; 64 KD PROTEIN [Rattus norvegicus]	AA058664	RC_AA058664	1.5	4.6
ESTs	R51913	RC_R51913	1.3	4.6
protein tyrosine phosphatase type IVA; member 2	AA329274	AA329274_f	1.9	4.6
calumenin	W84712	RC_W84712	3.5	4.6
ESTs	AA173597	AA173597	1.8	4.6
H.sapiens mRNA for Fas/Apo-1 (clone pCRTM11-Fasdelta(4,7))	X83492	X83492	0.8	4.6
ESTs	AA404427	RC_AA404427	1.3	4.6
ESTs	W65477	RC_W65477	1.2	4.6
ESTs	AA040270	RC_AA040270	1.3	4.6
hemoglobin; gamma A	R92458	RC_R92458_f	0.5	4.6
ESTs	F01831	RC_F01831	0.2	4.6
ESTs	Z41372	RC_Z41372_s	2.0	4.6
ESTs; Weakly similar to PROBABLE ATP-DEPENDENT RNA HELICASE HRH1 [H.sapiens]	AA410336	RC_AA410336	2.0	4.6
ESTs; Highly similar to GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 2 [Saccharomyces cerevisiae]	AA010686	AA010686	1.6	4.6
ESTs; Weakly similar to keratin 1 [H.sapiens]	AA037386	RC_AA037386_s	1.1	4.6
H1 histone family; member 2	T90190	RC_T90190_s	1.5	4.5
lysozyme (renal amyloidosis)	X14008	X14008_rna1_f	0.9	4.5
ESTs	Z39622	RC_Z39622_s	2.1	4.5
ribosomal protein L22	T23926	RC_T23926	1.5	4.5
tumor necrosis factor (ligand) superfamily; member 1	H25836	RC_H25836	3.2	4.5
ESTs	R60952	RC_R60952_i	1.0	4.5
Homo sapiens clone 23836 mRNA sequence	T17428	RC_T17428_s	1.0	4.5
NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 7 (18kD; B18)	AA609299	RC_AA609299_s	1.1	4.5
SET PROTEIN	AA205665	RC_AA205665_s	1.7	4.5
Human mRNA for KIAA349 gene; partial cds	AB002347	AB002347	0.7	4.5
protease; serine; 11 (IGF binding)	T82292	RC_T82292_s	2.1	4.5
ESTs	AA465218	RC_AA465218	1.6	4.5
ESTs	AA236018	RC_AA236018	1.2	4.5
SRY (sex determining region Y)-box 4	AA479953	RC_AA479953	8.7	4.5
LIVER CARBOXYLESTERASE PRECURSOR	T68878	RC_T68878_f	0.3	4.4
Human mRNA for KIAA228 gene; partial cds	AA431206	RC_AA431206_s	1.5	4.4
ESTs	AA489012	RC_AA489012	2.4	4.4
ESTs; Highly similar to NUCLEAR FACTOR 1 A1 [Gallus gallus]	F08945	RC_F08945	1.5	4.4
zinc finger protein 27	H80409	RC_H80409	1.5	4.4
ESTs	T86337	RC_T86337	1.2	4.4
ESTs	AA459245	RC_AA459245	0.9	4.4
ribosomal protein L22	N93380	RC_N93380	1.3	4.4
ATPase; Ca++ transporting; cardiac muscle; slow twitch 2	W61297	RC_W61297	0.4	4.4
ESTs	AA291749	RC_AA291749_s	4.4	4.4
tubulin; beta polypeptide	T03651	RC_T03651_s	1.0	4.4
regulator of G-protein signalling 5	AA348466	RC_AA348466_s	1.4	4.4

FIGURE 8 (Cont.)

ESTs; Highly similar to ARGINYL-TRNA SYNTHETASE; MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]	R12777	RC_R12777_s	1.5	4.4
cytochrome c oxidase subunit VIIb	Z14244	Z14244	0.9	4.4
ESTs	T92718	RC_T92718	1.1	4.3
protein phosphatase 2; regulatory subunit B (B56); delta isoform	T96379	RC_T96379_s	1.4	4.3
LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 1 PRECURSOR	T74571	RC_T74571_s	1.2	4.3
immunoglobulin lambda-like polypeptide 2	M34516	M34516_r	1.1	4.3
ESTs; Moderately similar to unknown [H.sapiens]	N23222	RC_N23222	2.2	4.3
ESTs	Z38688	RC_Z38688	0.3	4.3
ESTs	W42412	RC_W42412	1.1	4.3
ESTs; Highly similar to HEMOPOIETIC-SPECIFIC EARLY RESPONSE PROTEIN [Mus musculus]	W20487	RC_W20487_s	1.4	4.3
ESTs	N21407	RC_N21407	1.8	4.3
ESTs; Weakly similar to deduced amino acid sequence is highly homologous to hypothetical proteins of C.elegans(T23g5.4 and T23G5.2). [H.sapiens]	H97159	RC_H97159	1.2	4.3
poly (ADP-ribose) glycohydrolase	R69293	RC_R69293	1.0	4.3
ESTs	AA253459	RC_AA253459	0.9	4.3
ESTs	AA452248	RC_AA452248	0.9	4.3
Homo sapiens clone 23742 mRNA; partial cds	AA608649	RC_AA608649	1.2	4.3
ESTs; Highly similar to (defline not available 446693) [H.sapiens]	AA393432	AA393432_s	1.5	4.3
ESTs	AA398318	RC_AA398318	1.5	4.3
H.sapiens mRNA for translin associated zinc finger protein-1	R79723	RC_R79723_s	1.5	4.3
ESTs	Z38874	RC_Z38874	1.1	4.3
testis enhanced gene transcript	AA079500	RC_AA079500	1.1	4.3
ESTs	N48000	RC_N48000	2.7	4.3
von Hippel-Lindau syndrome	W31600	RC_W31600_f	2.3	4.3
ESTs	AA156230	RC_AA156230	1.0	4.3
v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog	H69138	RC_H69138	0.9	4.3
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	T34527	T34527	2.6	4.3
ESTs; Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]	AA029288	RC_AA029288	1.5	4.2
ESTs	AA458959	RC_AA458959	1.7	4.2
ESTs	T10108	RC_T10108_s	1.4	4.2
ESTs	H04753	RC_H04753_f	3.2	4.2
ras homolog gene family; member H	W63747	RC_W63747	1.8	4.2
Homo sapiens voltage dependent anion channel protein mRNA; complete cds	AA094989	AA094989	0.7	4.2
ESTs; Weakly similar to Bat2 [H.sapiens]	H05631	RC_H05631_f	1.2	4.2
ESTs	R44357	RC_R44357	1.8	4.2
ESTs	N34482	RC_N34482	1.4	4.2
Microfibril-associated glycoprotein-2	U37283	U37283	1.1	4.2
ESTs; Weakly similar to CH-TOG PROTEIN [H.sapiens]	AA418985	RC_AA418985	2.3	4.2
ESTs; Moderately similar to (defline not available 4589678) [H.sapiens]	AA252765	RC_AA252765	1.0	4.2
Homo sapiens mRNA for KIAA214 protein; complete cds	R24483	RC_R24483_s	0.6	4.2
zinc finger protein 262	AA481428	RC_AA481428	1.0	4.2
CAAX box 1	AA279811	RC_AA279811_s	0.9	4.2

FIGURE 8
(Cont.)

ESTs; Weakly similar to (defline not available 46333) [H.sapiens]	AA452082	AA452082	1.0	4.2
cytochrome b-561	T03441	RC_T03441_f	1.2	4.2
ESTs	AA040945	RC_AA040945	0.8	4.2
FSHD region gene 1	H82532	RC_H82532	1.1	4.2
ESTs	AA093977	AA093977	1.2	4.2
ESTs	R26589	RC_R26589_f	1.0	4.2
von Hippel-Lindau binding protein 1	U56833	U56833	1.4	4.2
S1 calcium-binding protein A8 (calgranulin A)	M21005	M21005	0.9	4.2
ESTs; Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]	W95592	RC_W95592_i	1.3	4.1
ESTs	AA620962	RC_AA620962	1.2	4.1
histatin 1	L05512	L05512	0.8	4.1
ESTs	AA293426	RC_AA293426	0.7	4.1
cyclin F	T89627	RC_T89627_s	1.3	4.1
ESTs; Weakly similar to Similarity to Serpentwood strictosidine synthase precursor [C.elegans]	AA256171	RC_AA256171	1.9	4.1
ESTs	AA311352	AA311352_s	1.6	4.1
ESTs	AA405654	RC_AA405654_s	1.5	4.1
ESTs; Highly similar to ACTIN II [Plasmodium falciparum]	AA040263	RC_AA040263	1.1	4.1
ESTs	C01552	C01552	1.0	4.1
ESTs; Weakly similar to KIAA319 [H.sapiens]	N95507	N95507	1.3	4.1
ESTs	N63706	RC_N63706	1.0	4.1
ESTs	AA152312	RC_AA152312	1.1	4.1
laminin; beta 1	M61916	M61916	1.5	4.1
ESTs	AA063431	RC_AA063431_f	0.8	4.1
ESTs	N39016	RC_N39016	1.3	4.1
ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	W45457	RC_W45457	1.2	4.1
ESTs	C15324	RC_C15324_f	4.2	4.1
ESTs	N46086	N46086_s	1.6	4.1
ESTs	W45494	RC_W45494	1.0	4.1
bone morphogenetic protein 6	AA598702	RC_AA598702	1.6	4.1
cadherin 11 (OB-cadherin; osteoblast)	D21254	D21254_s	3.2	4.1
ESTs; Weakly similar to ribokinase [E.coli]	T69020	RC_T69020_s	0.9	4.1
ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	AA120783	RC_AA120783	1.4	4.1
erythrocyte membrane protein band 7.2 (stomatin)	H27442	RC_H27442_s	1.0	4.1
solute carrier family 7 (cationic amino acid transporter; y+ system); member 6	R51116	RC_R51116_f	0.8	4.1
ESTs	T69728	RC_T69728	1.1	4.1
Homo sapiens clone 2377 mRNA sequence	R44163	RC_R44163_f	0.9	4.1
ESTs	W80739	RC_W80739_f	1.0	4.1
ESTs; Moderately similar to LNXp7 [M.musculus]	H82424	RC_H82424	1.7	4.0
secreted frizzled-related protein 4	AA487193	RC_AA487193	4.7	4.0
ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	AA428607	RC_AA428607	1.3	4.0
fumarylacetoacetate	W79422	RC_W79422_s	1.3	4.0
MATRIN 3	N20178	RC_N20178	1.2	4.0
ESTs	W67727	RC_W67727	1.4	4.0
ESTs	AA011510	RC_AA011510	1.8	4.0

FIGURE 8
(Cont.)

ESTs	AA069569	RC_AA069569	1.5	4.0
cysteine-rich protein 1 (intestinal)	N92934	RC_N92934_s	2.5	4.0
ESTs	AA004415	RC_AA004415	1.2	4.0
ESTs	W81205	RC_W81205	1.5	4.0
ESTs	N56993	RC_N56993	2.0	4.0
ESTs	AA256943	RC_AA256943_s	0.8	4.0
ESTs	N68133	RC_N68133	0.7	4.0
homogentisate 1;2-dioxygenase (homogentisate oxidase)	R08615	RC_R08615_s	0.5	4.0
Meis1 (mouse) homolog	N95243	RC_N95243_s	0.9	4.0
Accession not listed in Genbank	K01160	K01160	1.7	4.0
ESTs	T33489	RC_T33489_s	1.3	4.0
H2A histone family; member Z	M37583	M37583	2.8	4.0
B-factor; properdin	T72268	RC_T72268_s	1.3	4.0
ESTs	AA133457	RC_AA133457	1.2	4.0
ESTs	AA287681	RC_AA287681_s	1.3	4.0
ESTs; Highly similar to HYPOTHETICAL 84.7 KD PROTEIN ZK198.1 IN CHROMOSOME III [Caenorhabditis elegans]	AA481403	RC_AA481403	4.0	4.0
ESTs	AA233445	RC_AA233445	1.9	4.0
ESTs; Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens]	AA452256	RC_AA452256	1.2	4.0
ESTs; Weakly similar to deduced amino acid sequence is highly homologous to hypothetical proteins of C.elegans(T23g5.4 and T23G5.2). [H.sapiens]	AA488433	RC_AA488433	1.1	4.0
Homo sapiens mRNA for KIAA719 protein; complete cds	R60689	RC_R60689	1.9	4.0
ESTs	AA016306	RC_AA016306	0.6	4.0
H.sapiens mRNA for nuclear protein SA-2	AA489057	RC_AA489057	6.2	4.0
ESTs	AA431191	RC_AA431191_s	1.8	4.0
protein kinase C; zeta	R24258	RC_R24258_s	0.7	4.0
ESTs	N66847	RC_N66847	1.4	4.0
ESTs	AA233548	RC_AA233548	1.5	4.0
ESTs	AA400229	RC_AA400229	1.7	4.0
ESTs; Weakly similar to SAS [H.sapiens]	H07011	H07011	1.8	3.9
Human mRNA for KIAA96 gene; partial cds	D60769	RC_D60769_s	0.9	3.9
cell division cycle 42 (GTP-binding protein; 25kD)	AA031548	AA031548	3.1	3.9
ESTs	H29293	RC_H29293_f	1.6	3.9
Rho GTPase activating protein 1	AA032067	RC_AA032067_s	2.0	3.9
ESTs; Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos taurus]	AA234533	AA234533	1.4	3.9
calpain; large polypeptide L2	R39610	RC_R39610_s	1.3	3.9
ESTs	AA456845	RC_AA456845	1.4	3.9
ESTs; Highly similar to ATP SYNTHASE EPSILON CHAIN; MITOCHONDRIAL PRECURSOR [Bos taurus]	W72685	RC_W72685	1.3	3.9
Homo sapiens mRNA for KIAA886 protein; complete cds	W58081	RC_W58081	1.0	3.9
ESTs; Highly similar to (defline not available 467918) [H.sapiens]	AA026962	RC_AA026962	1.4	3.9
Human DNA from overlapping chromosome 19 cosmids R31396; F25451; and R3176 containing COX6B and UPKA; genomic sequence	T15852	RC_T15852_f	2.0	3.9
ESTs	AA256317	RC_AA256317	1.3	3.9
ESTs	AA504492	RC_AA504492	2.4	3.9
ESTs	R78224	RC_R78224	1.0	3.9
ESTs	W74728	RC_W74728	0.2	3.9

FIGURE 8
(Cont.)

Human mRNA for KIAA263 gene; complete cds	T90946	RC_T90946_f	1.1	3.9
ESTs	D59711	RC_D59711_f	2.6	3.9
ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	AA428364	RC_AA428364_s	1.3	3.9
ESTs	AA342457	RC_AA342457_i	2.1	3.9
ATPase; H+ transporting; lysosomal (vacuolar proton pump) 9kD	AA214710	AA214710	1.4	3.9
Homo sapiens mRNA for nuclear protein; NP22; complete cds	AA147532	RC_AA147532_s	2.8	3.9
Homo sapiens mRNA for KIAA75 protein; complete cds	AA157623	AA157623_s	1.2	3.9
ESTs	T90345	RC_T90345	1.2	3.9
ESTs	AA410424	RC_AA410424	1.3	3.9
ESTs; Highly similar to (defline not available 467914) [H.sapiens]	N26691	RC_N26691	1.6	3.9
Homo sapiens mRNA for KIAA99 protein; partial cds	N51651	RC_N51651	0.9	3.9
ESTs; Highly similar to MICROSOMAL SIGNAL PEPTIDASE 21 KD SUBUNIT [Canis familiaris]	AA234347	RC_AA234347	1.3	3.9
ATPase; H+ transporting; lysosomal (vacuolar proton pump); beta polypeptide; 56/58kD; isoform 2	M60346	M60346_s	0.9	3.9
RAB4; member RAS oncogene family	X82554	X82554_rna1	0.8	3.9
ESTs; Highly similar to TISSUE ALPHA-L-FUCOSIDASE PRECURSOR [Homo sapiens]	AA234925	RC_AA234925	1.4	3.9
heterogeneous nuclear ribonucleoprotein A2/B1	AA131165	RC_AA131165_s	2.0	3.9
Human mariner-like element-containing mRNA; clone pcHMT1	AA487508	RC_AA487508	1.9	3.9
ESTs	AA489618	RC_AA489618_s	1.5	3.9
ESTs	AA436158	RC_AA436158	3.9	3.9
ESTs	AA256688	RC_AA256688_s	1.0	3.8
ESTs	H14982	RC_H14982_r	1.0	3.8
ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)	J03473	J03473	2.1	3.8
ESTs	W60310	RC_W60310	1.3	3.8
ESTs	AA040397	RC_AA040397	1.5	3.8
ESTs	T15457	RC_T15457_f	1.0	3.8
ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	N67343	RC_N67343	2.1	3.8
ESTs; Highly similar to HYPOTHETICAL 3.5 KD PROTEIN C3A5.3 IN CHROMOSOME III [Caenorhabditis elegans]	AA348925	RC_AA348925_s	2.4	3.8
protocadherin 2 (cadherin-like 2)	T65540	RC_T65540_s	1.0	3.8
ESTs	AA404421	RC_AA404421	1.2	3.8
ESTs	AA237009	RC_AA237009	1.3	3.8
ESTs; Moderately similar to ATP-CITRATE [Rattus norvegicus]	D51405	RC_D51405	1.4	3.8
Human Ig J chain gene	M12759	M12759	0.5	3.8
ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]	H90314	RC_H90314_s	1.2	3.8
NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase)	AA063581	RC_AA063581	0.8	3.8
H.sapiens OZF mRNA	T25747	RC_T25747_s	1.8	3.8
lumican	U21128	U21128	2.2	3.8
heterogeneous nuclear ribonucleoprotein G	AA173143	RC_AA173143_s	1.6	3.8
ESTs	N63165	RC_N63165	1.1	3.8
ESTs; Weakly similar to KIAA62 [H.sapiens]	AA233763	RC_AA233763	0.6	3.8
Human high density lipoprotein binding protein (HBP) mRNA; complete cds	H28100	RC_H28100_s	1.9	3.8
ESTs	AA074350	RC_AA074350	1.3	3.8
ESTs	W46632	RC_W46632	1.1	3.8

FIGURE 8
(Cont.)

ESTs	AA491278	RC_AA491278_r	1.0	3.8
ESTs; Highly similar to GASTRULA ZINC FINGER PROTEIN XLCGF8.2DB [Xenopus laevis]	T58753	RC_T58753_f	1.4	3.8
Homo sapiens lysophospholipase (LPL1) mRNA; complete cds	AA251902	RC_AA251902	2.2	3.8
interferon stimulated gene (2kD)	AA504805	RC_AA504805_s	1.3	3.8
Homo sapiens mRNA for KIAA446 protein; complete cds	AA416723	RC_AA416723	1.0	3.8
Homo sapiens mRNA for KIAA92 protein; complete cds	T65396	RC_T65396_f	1.0	3.8
ESTs; Weakly similar to alternatively spliced product using exon 13A [H.sapiens]	H95569	RC_H95569_i	0.5	3.7
ESTs; Highly similar to ZINC FINGER PROTEIN ZFP-92 [Mus musculus]	T26494	RC_T26494_f	1.3	3.7
ESTs	AA174183	AA174183_s	2.0	3.7
cellular retinoic acid-binding protein 1	R53950	RC_R53950_s	1.1	3.7
erythrocyte membrane protein band 4.1-like 2	AA427955	RC_AA427955	0.5	3.7
ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	AA425378	RC_AA425378_r	0.9	3.7
yd73e9.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113896 3', mRNA sequence	T77525	RC_T77525	1.5	3.7
ESTs	AA477445	RC_AA477445	1.4	3.7
ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	AA071089	RC_AA071089	1.2	3.7
ferritin; light polypeptide	T63769	RC_T63769_f	1.1	3.7
ESTs	R63173	RC_R63173_s	2.0	3.7
Homo sapiens mRNA for DnaJ protein	W72906	RC_W72906	2.7	3.7
ESTs	R32393	RC_R32393_s	1.2	3.7
Homo sapiens mRNA for KIAA878 protein; complete cds	H98653	RC_H98653	2.8	3.7
procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	U84573	U84573	1.8	3.7
ESTs	AA156335	RC_AA156335	4.6	3.7
zn13d5.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:54735 3' similar to gb:L8441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);, mRNA sequence	AA085374	RC_AA085374	1.6	3.7
fibroblast growth factor receptor 2 (bacteria-expressed kinase; keratinocyte growth factor receptor; craniofacial dysostosis 1; Crouzon syndrome; Pfeiffer syndrome; Jackson-Weiss syndrome)	AA489375	RC_AA489375_f	1.6	3.7
ESTs; Weakly similar to eyelid [D.melanogaster]	Z38897	RC_Z38897_s	1.2	3.7
ESTs	AA235040	RC_AA235040	1.5	3.7
collagen; type III; alpha 1 (Ehlers-Danlos syndrome type IV; autosomal dominant)	X06700	X06700	4.7	3.7
ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]	T26471	RC_T26471	4.5	3.7
ESTs	R27006	RC_R27006_f	1.6	3.7
H.sapiens mRNA for putative progesterone binding protein	H60595	RC_H60595_s	1.3	3.7
fibroblast growth factor receptor 2 (bacteria-expressed kinase; keratinocyte growth factor receptor; craniofacial dysostosis 1; Crouzon syndrome; Pfeiffer syndrome; Jackson-Weiss syndrome)	AA460450	RC_AA460450	1.5	3.7
ATPase; H+ transporting; lysosomal (vacuolar proton pump); alpha polypeptide; 7kD; isoform 1	AA228122	RC_AA228122	1.1	3.7
ribosomal protein; large; P	AA416866	RC_AA416866_f	1.3	3.7
ESTs	R21443	R21443	1.6	3.7
Homo sapiens mRNA for KIAA564 protein; partial cds	AA053020	RC_AA053020_i	1.0	3.7

FIGURE 8
(Cont.)

ESTs; Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]	N91377	RC_N91377	2.8	3.7
ESTs	H95989	RC_H95989_s	2.0	3.7
ESTs; Weakly similar to B-cell growth factor [H.sapiens]	T88817	RC_T88817	1.0	3.7
ESTs; Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN SUI2-TDH2 INTERGENIC REGION [Saccharomyces cerevisiae]	AA394126	RC_AA394126	1.8	3.6
ESTs	R38547	RC_R38547	0.9	3.6
ESTs; Weakly similar to uroporphyrinogen III synthase; UROIIIS [H.sapiens]	AA476237	RC_AA476237	1.5	3.6
ESTs	R53062	RC_R53062	0.8	3.6
ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]	AA452237	RC_AA452237_i	3.6	3.6
ESTs; Weakly similar to hypothetical protein [H.sapiens]	AA040465	RC_AA040465	1.2	3.6
ESTs	AA350781	RC_AA350781	1.1	3.6
ESTs	AA121313	RC_AA121313	1.4	3.6
ESTs	AA234966	RC_AA234966	1.6	3.6
ESTs	W58461	RC_W58461	1.0	3.6
ESTs	AA252372	RC_AA252372	1.2	3.6
ESTs	W31470	RC_W31470	1.5	3.6
ESTs; Weakly similar to hypothetical protein [H.sapiens]	D80076	RC_D80076_f	1.7	3.6
ubiquitin specific protease 7 (herpes virus-associated)	R54935	RC_R54935_s	1.7	3.6
ESTs; Weakly similar to SH3BGR PROTEIN [H.sapiens]	D30930	D30930_s	1.1	3.6
Homo sapiens mRNA for low molecular mass ubiquinone-binding protein; complete cds	N77716	N77716_s	1.2	3.6
ESTs; Weakly similar to alternatively spliced product using exon 13A [H.sapiens]	R56485	RC_R56485	1.0	3.6
ESTs	AA135894	RC_AA135894	1.3	3.6
zm97f8.s1 Stratagene colon HT29 (#937221) Homo sapiens cDNA clone IMAGE:545895 3', mRNA sequence	AA079487	RC_AA079487	1.5	3.6
ESTs	N22152	RC_N22152_f	1.9	3.6
ESTs	AA114893	RC_AA114893	1.2	3.6
Homo sapiens HRIHFB2115 mRNA; partial cds	AA278400	RC_AA278400_f	1.5	3.6
ESTs; Weakly similar to similar to SP:YR4_BACSU [C.elegans]	W67789	RC_W67789	1.2	3.6
ESTs; Weakly similar to cDNA EST EMBL:C1359 comes from this gene [C.elegans]	N89819	RC_N89819	1.4	3.6
ESTs; Moderately similar to (defline not available 446549) [H.sapiens]	AA488658	RC_AA488658	2.4	3.6
Human clone 121711 defective mariner transposon Hsmar2 mRNA sequence	H88535	RC_H88535_f	1.3	3.6
ESTs	AA459255	RC_AA459255	1.3	3.6
immunoglobulin gamma 3 (Gm marker)	M87789	M87789	1.2	3.6
Homo sapiens signalosome subunit 2 (SGN2) mRNA; complete cds	AA458919	RC_AA458919	1.2	3.6
sorting nexin 3	W49551	RC_W49551	1.2	3.6
ESTs; Highly similar to (defline not available 3915613) [H.sapiens]	W38597	W38597_s	1.1	3.6
ESTs	AA446451	RC_AA446451	1.1	3.6
hemoglobin; gamma A	H74317	RC_H74317_s	0.2	3.6
neuromedin B	X76534	X76534	2.2	3.6
ESTs; Highly similar to 26S PROTEASE REGULATORY SUBUNIT 6 [Homo sapiens]	AA441978	RC_AA441978	1.2	3.6
ESTs; Moderately similar to histone H2B [H.sapiens]	AA610040	RC_AA610040	1.1	3.6
Homo sapiens clone 2477 mRNA sequence	T15703	RC_T15703	1.4	3.6

FIGURE 8
(Cont.)

Human glutamate dehydrogenase (GDH) mRNA; complete cds	T86978	RC_T86978_s	1.0	3.6
Homo sapiens mRNA for leptin receptor gene-related protein	AA393825	RC_AA393825	1.1	3.6
ESTs	R49385	RC_R49385	1.5	3.6
ESTs	W16996	W16996_s	1.1	3.6
ESTs	AA351254	RC_AA351254	0.9	3.6
ESTs; Weakly similar to neuronal tyrosine threonine phosphatase 1 [M.musculus]	T88897	RC_T88897	0.9	3.6
ESTs	N70873	RC_N70873	1.1	3.5
ESTs	AA236532	RC_AA236532_s	1.0	3.5
APOLIPOPROTEIN AI REGULATORY PROTEIN-1	AA393876	RC_AA393876_s	0.9	3.5
ESTs	AA027229	RC_AA027229	1.3	3.5
ESTs; Weakly similar to The KIAA147 gene product is related to adenylyl cyclase. [H.sapiens]	AA131394	RC_AA131394	1.4	3.5
ESTs	AA235505	RC_AA235505	1.4	3.5
ESTs	N21207	RC_N21207	1.6	3.5
protease; serine; 11 (IGF binding)	D87258	D87258	2.4	3.5
Homo sapiens SNC73 protein (SNC73) mRNA; complete cds	H27498	RC_H27498_f	1.1	3.5
ESTs	AA621788	RC_AA621788	1.1	3.5
Human mRNA for KIAA249 gene; complete cds	T95515	RC_T95515_s	1.6	3.5
ESTs	AA043960	RC_AA043960	1.1	3.5
ribosomal protein; large; P	W32281	RC_W32281_f	1.3	3.5
ESTs; Highly similar to POTASSIUM CHANNEL PROTEIN KV2.1 [Rattus norvegicus]	T89084	RC_T89084	1.0	3.5
ESTs	T52700	RC_T52700	0.9	3.5
ESTs	H16772	RC_H16772	1.2	3.5
ATP synthase; H+ transporting; mitochondrial F complex; subunit c (subunit 9) isoform 3	AA112059	RC_AA112059_s	1.1	3.5
ESTs; Highly similar to HYPOTHETICAL 17.2 KD PROTEIN F44E2.6 IN CHROMOSOME III [Caenorhabditis elegans]	R49920	RC_R49920	1.5	3.5
ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	N54909	RC_N54909_s	2.3	3.5
ESTs	AA033974	RC_AA033974	1.6	3.5
ESTs; Weakly similar to Weak similarity with Salmonella typhimurium RFBU protein [C.elegans]	AA057832	RC_AA057832	1.2	3.5
synaptophysin	R42172	RC_R42172	0.6	3.5
ESTs	W27770	W27770	0.9	3.5
EST	AA164676	RC_AA164676	1.2	3.5
ESTs; Highly similar to THROMBOXANE A2 RECEPTOR [Homo sapiens]	AA253424	RC_AA253424	1.0	3.5
ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	N23761	RC_N23761	1.8	3.5
GLUCOSYLCERAMIDASE PRECURSOR	T48672	RC_T48672_s	1.1	3.5
collagen; type VI; alpha 3	X52022	X52022	2.6	3.5
ESTs; Highly similar to HYPOTHETICAL 44.2 KD PROTEIN IN SCO2-MRF1 INTERGENIC REGION [Saccharomyces cerevisiae]	T35725	T35725_s	2.1	3.5
ESTs; Weakly similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]	T40145	T40145	1.1	3.5
Human mRNA for KIAA9 gene; complete cds	H86350	RC_H86350_s	1.3	3.5
ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	R81173	RC_R81173	1.3	3.5
fatty-acid-Coenzyme A ligase; long-chain 3	AA316272	AA316272	1.7	3.5
ESTs	R46209	RC_R46209	1.4	3.5

FIGURE 8
(Cont.)

ESTs	AA397916	RC_AA397916_i	1.4	3.5
ESTs	T89379	RC_T89379	1.1	3.5
ESTs	H98714	RC_H98714_s	1.6	3.5
ESTs	N69552	RC_N69552	1.2	3.5
Human alpha satellite and satellite 3 junction DNA sequence	M21305	M21305	29.9	0.3
transcription factor AP-2 alpha (activating enhancer-binding protein 2 alpha)	AA458761	AA458761_i	13.9	0.8
Prolactin-Induced Protein	HG1763-HT1780	HG1763-HT1780	11.9	0.4
ESTs	AA164586	RC_AA164586_s	6.2	0.8
Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA; partial cds	AA447146	RC_AA447146_s	5.9	1.6
H4 histone family; member G	X60486	X60486	5.8	1.5
ESTs	AA424798	RC_AA424798	5.5	2.9
ESTs	AA425309	RC_AA425309	5.4	1.2
ESTs	R55185	RC_R55185	5.3	1.2
Homo sapiens mRNA for KIAA48 protein; complete cds	AA412149	RC_AA412149	5.0	2.0
ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	AA621557	RC_AA621557	5.0	1.3
desmoplakin (DPI; DPII)	W95070	RC_W95070	5.0	2.6
ESTs	R49482	RC_R49482	4.6	2.0
ESTs	AA406145	RC_AA406145_f	4.6	3.0
dual specificity phosphatase 4	U48807	U48807	4.5	0.5
ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	N22107	RC_N22107	4.5	2.4
golgi SNAP receptor complex member 1	AA481414	RC_AA481414	4.4	0.9
Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA; partial cds	U28831	U28831	4.4	0.6
matrix metalloproteinase 7 (matrilysin; uterine)	L22524	L22524	4.4	0.6
Homo sapiens clone 24629 mRNA sequence	AA419386	RC_AA419386	4.3	1.3
EST	W86779	RC_W86779	4.3	0.7
ser-Thr protein kinase related to the myotonic dystrophy protein kinase	N39214	RC_N39214	4.3	0.5
ESTs	T10100	RC_T10100_f	4.3	0.9
ESTs	AA251297	RC_AA251297	4.3	2.9
mammaglobin 1	U33147	U33147	4.2	0.7
ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]	N66845	RC_N66845	4.2	0.5
Sjogren syndrome antigen A2 (6kD; ribonucleoprotein autoantigen SS-A/Ro)	AA075182	RC_AA075182	4.2	2.0
ESTs	AA411621	RC_AA411621	4.1	1.2
ESTs	AA255933	RC_AA255933	4.0	1.4
ESTs	H88496	H88496_s	4.0	1.3
Protein Kinase Ht31, Camp-Dependent	HG2167-HT2237	HG2167-HT2237	3.8	1.2
prolactin-induced protein	J03460	J03460_s	3.8	0.6
ESTs	W81552	RC_W81552	3.8	1.0
ESTs	AA398892	RC_AA398892	3.8	1.9
X-box binding protein 1	M31627	M31627	3.8	0.8
ESTs	H48032	RC_H48032	3.7	3.3
protein tyrosine phosphatase; receptor type; F	Y00815	Y00815	3.7	1.2
homolog of mouse quaking QKI (KH domain RNA binding protein)	AA280004	RC_AA280004	3.7	1.5
ESTs	F10707	RC_F10707	3.7	1.3

FIGURE 8
(Cont.)

ESTs	AA255991	RC_AA255991	3.7	1.0
cadherin 3; P-cadherin (placental)	X63629	X63629	3.7	0.5
ESTs	N67149	RC_N67149	3.5	3.3
Homo sapiens CD24 signal transducer mRNA, complete cds and 3' region	L33930	L33930	3.5	1.1
copine III	W86835	RC_W86835	3.5	1.9
Homo sapiens mRNA for semaphorin E; complete cds	AA042990	RC_AA042990_s	3.5	1.0
Homo sapiens clone 23967 unknown mRNA; partial cds	AA070485	RC_AA070485	3.4	2.6
Homo sapiens mRNA for KIAA882 protein; partial cds	Z39762	RC_Z39762_s	3.4	0.9
ESTs	AA419622	RC_AA419622	3.4	3.2
SRY (sex determining region Y)-box 4	AA458584	AA458584	3.4	0.4
Human gastrointestinal tumor-associated antigen GA733-1 protein gene, complete cds, clone 5516	J04152	J04152_rna1	3.4	0.4
ESTs; Highly similar to RING3 PROTEIN [Homo sapiens]	AA188647	RC_AA188647	3.3	2.8
ESTs; Weakly similar to Numblike [M.musculus]	AA463254	RC_AA463254_s	3.3	1.6
wee1+ (S. pombe) homolog	T16282	RC_T16282_f	3.3	1.1
SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 4	U29175	U29175	3.3	3.4
Homo sapiens mRNA for squalene epoxidase, partial cds	D78129	D78129	3.3	1.4
ESTs	AA456687	AA456687	3.3	2.2
ESTs; Weakly similar to NF-kB subunit [H.sapiens]	AA487561	RC_AA487561	3.3	1.2
hepatocyte growth factor activator inhibitor	AA157857	RC_AA157857_s	3.3	2.4
MITOCHONDRIAL 6S RIBOSOMAL PROTEIN L3	X06323	X06323	3.3	2.1
ESTs	AA496053	RC_AA496053	3.3	1.8
ESTs	AA058846	RC_AA058846	3.3	3.3
ESTs; Highly similar to N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG [Leishmania donovani]	C02582	C02582	3.3	3.3
stanniocalcin 2	AA126474	RC_AA126474	3.2	0.2
STATHMIN	D51276	RC_D51276_f	3.2	3.0
collagen; type I; alpha 1	Z74615	Z74615	3.2	3.0
ESTs	AA485431	RC_AA485431_s	3.2	2.4
ESTs	H89575	H89575_s	3.2	0.6
ESTs	T17185	RC_T17185	3.2	3.0
ESTs	R39044	RC_R39044	3.2	0.8
ESTs	D60411	RC_D60411_s	3.2	0.8
ESTs; Weakly similar to ubiquitous TPR motif; Y isoform [H.sapiens]	T91518	RC_T91518_f	3.2	2.5
3-prime-phosphoadenosine 5-prime-phosphosulfate synthase 1	AA165526	RC_AA165526	3.2	1.8
androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)	M35851	M35851	3.2	1.8
Human mRNA for calgizzarin; complete cds	D38583	D38583	3.2	2.3
Human 26S proteasome-associated pad1 homolog (POH1) mRNA; complete cds	AA621752	RC_AA621752	3.2	2.5
heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	R99599	RC_R99599_s	3.2	3.4
ESTs	AA088228	RC_AA088228	3.2	1.4
ESTs	W72838	RC_W72838	3.2	1.0
ESTs	AA485212	RC_AA485212	3.1	1.4
keratin 19	Y00503	Y00503	3.1	1.1
collagen; type XV; alpha 1	L25286	L25286	3.1	3.4
ESTs; Weakly similar to predicted using Genefinder [C.elegans]	AA416886	RC_AA416886	3.1	3.1

FIGURE 8
(Cont.)

ESTs	AA406294	RC_AA406294	3.1	3.1
Human alpha-1 collagen type I gene, 3' end	M55998	M55998	3.1	1.7
ESTs	W02734	RC_W02734	3.1	1.4
KERATIN; TYPE II CYTOSKELETAL 7	M13955	M13955	3.1	1.1
H.sapiens mRNA for retrotransposon	AA598453	RC_AA598453_s	3.1	0.7
ESTs; Weakly similar to DREBRINS E1 AND E2 [Gallus gallus]	N69879	RC_N69879_s	3.1	1.6
ESTs	N48603	RC_N48603	3.1	1.2
ESTs; Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]	N51488	RC_N51488	3.0	1.6
ESTs; Weakly similar to 25 kDa trypsin inhibitor [H.sapiens]	N67422	RC_N67422_s	3.0	1.5
ESTs; Highly similar to 6S RIBOSOMAL PROTEIN L3A [Saccharomyces cerevisiae]	AA045365	RC_AA045365	3.0	1.7
ESTs	T32108	RC_T32108	3.0	1.1
ESTs; Weakly similar to FUN9 transcript; essential gene; similar to Schizosaccharomyces pombe unknown orf SPAC24B11.8c; GenBank Accession Number Z67757 [S.cerevisiae]	AA504631	RC_AA504631	3.0	3.0

FIGURE 8
(Cont.)

Accession	Title
Z29083	5T4 Oncofetal antigen
AA443962	Homo sapiens histone acetyltransferase (HBO1) mRNA, complete cds
AA055656	ESTs
D20342	transducer of erbB-2 (TOB)
AA130273	ESTs; Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]
U23070	Human putative transmembrane protein (nma) mRNA; complete cds
AA235448	ESTs
AA256162	ESTs
AA436880	ESTs; Moderately similar to similar to rat integral membrane glycoprotein; PIR Accession Number A467 [H.sapiens]
AA256485	ESTs

FIGURE 9

FIGURE 10

Accession	UniGene ID	UniGene Title		ratio tumor/ body	90%tile tumor	75%tile body	ratio tumor/ normal breast
AA126474	Hs.155223	stanniocalcin 2		72.2	722	1	1.9
U20758	Hs.313	secreted phosphoprotein 1 (osteopontin; bone sialoprotein		45.7	457	1	39.7
AA434329	Hs.36563	ESTs	BCJ7	40.2	402	1	4
AA250737	Hs.72472	ESTs	BCY2	35.9	359	10	29.7
X82153	Hs.83942	cathepsin K (pycnodysostosis)		34.3	411	12	5.1
X03635	Hs.1657	estrogen receptor 1	BCQ3	32.2	322	1	4.7
H09290	Hs.76550	ESTs; Weakly similar to unknown [H.sapiens]		30.6	306	4	26.5
AA428090	Hs.26102	ESTs	BCN2	29	290	1	26.8
AA419547	Hs.11713	ESTs		26.3	356	14	1
AA256485	Hs.182471	ESTs	BCO2	25.4	508	20	3
N67239	Hs.10760	ESTs	BCX9	25.1	288	12	6.7
Z38595	Hs.125019	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING	BCY3	24.2	242	10	5.6
H25836	Hs.83429	tumor necrosis factor (ligand) superfamily; member 10		22.8	228	9	12.4
HG1763-HT1780		Prolactin-Induced Protein		22.7	760	34	1.4
C01714	Hs.3838	serum-inducible kinase		22.6	226	10	0.9
U28686	Hs.182225	RNA binding motif protein 3		22.1	221	9	17.8
AA411621	Hs.8895	ESTs		21.2	212	6	17.4
N46252	Hs.29724	ESTs	BCX6	20.9	209	1	19.5
U05237	Hs.99872	fetal Alzheimer antigen		20.6	206	4	19.1
U48807	Hs.2359	dual specificity phosphatase 4		20.2	202	5	1.3
AA070801	Hs.51615	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNI		18.7	187	1	17
U28831	Hs.44566	Human protein immuno-reactive with anti-PTH polyclonal		18.6	186	10	1.5
AA292066	Hs.240802	ESTs; Weakly similar to Br140 [H.sapiens]		17.5	175	2	12.8
AA291725	Hs.105700	secreted frizzled-related protein 4	BCX2	17.4	409	24	7.8
N26722	Hs.42645	ESTs	BCY5	17.4	174	9	6.9
AA256323	Hs.25264	ESTs		16.6	166	8	12.7
AA065217	Hs.169674	ESTs		16.2	162	1	4.2
AA446650	Hs.27860	ESTs		16	255	16	6.6
D13666	Hs.136348	osteoblast specific factor 2 (fasciclin I-like)	BCA4	15.7	1030	66	5
AA621169	Hs.8687	ESTs	BCX8	15.6	156	7	10.8
L07615		"Human neuropeptide Y receptor Y1 (NPYY1) mRNA, exo		15.3	153	1	14.1
AA456598	Hs.240190	ESTs		15.2	152	1	12.6
AA007234	Hs.30098	ESTs		14.9	149	1	6.4
F01831	Hs.14838	ESTs	BCX4	14.6	219	15	7.6
N66818	Hs.42179	ESTs	BCY6	14.5	145	1	2.4
HG2167-HT2237		"Protein Kinase Ht31, Camp-Dependent"		14.4	144	9	4.7
Z39821	Hs.107295	ESTs		14.3	143	9	13.1
H05509	Hs.24639	ESTs		14.2	142	1	9.5
T90621	Hs.109052	chromosome 14 open reading frame 2		14.2	142	6	9.4
AA171913	Hs.5338	carbonic anhydrase XII		14.2	390	28	22.5
AA149007	Hs.243954	ESTs		13.7	137	1	8.9
N22222		"yw34b06.s1 Morton Fetal Cochlea Homo sapiens cDNA		13.5	135	1	5.1
AA480975	Hs.44829	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WA		13.3	133	8	3.2
D62633	Hs.8236	ESTs		13.3	445	34	6
D12485	Hs.11951	phosphodiesterase I/nucleotide pyrophosphatase 1 (homo	BCA2	13.2	244	19	9.9
AA490262	Hs.15485	ESTs; Moderately similar to APXL gene product [H.sapien	BCU8	13.2	331	25	12.4
W93640	Hs.4779	ESTs		13.1	131	1	5.1
D49396	Hs.75454	Human mRNA for Apo1_Human (MER5(Aop1-Mouse)-like		12.8	128	1	11.7
H94892	Hs.6906	v-ral simian leukemia viral oncogene homolog A (ras relat		12.8	141	11	12.2
AA458761	Hs.18387	ESTs		12.7	311	25	2.4
AA436158	Hs.190013	ESTs		12.6	126	7	7.5
AA444369	Hs.177537	ESTs		12.6	126	8	9.9
X14787	Hs.87409	thrombospondin 1		12.6	126	1	10.8
T40327	Hs.80680	ESTs		12.5	156	13	2.9
Z48633	Hs.6940	H.sapiens mRNA for retrotransposon		12.4	124	6	10.8
AA227219	Hs.110826	Homo sapiens CAGF9 mRNA; partial cds		12.3	123	1	11.3
T97307	Hs.161720	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARN		12.3	129	11	11.7

FIGURE 10
(CONT.)

M86849		"Homo sapiens connexin 26 (GJB2) mRNA, complete cds	CBC2	12	120	8	9
AA417152	Hs.5101	ESTs; Highly similar to protein regulating cytokinesis 1 [H.	CQA4	11.8	201	17	19.1
D31352	Hs.31433	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNI		11.7	117	1	10.1
AA251089	Hs.94576	ESTs; Weakly similar to phosducin; retinal [H.sapiens]		11.5	115	1	6.9
AA224180	Hs.187579	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING		11.5	115	1	10
F11019	Hs.12696	ESTs		11.4	114	1	10
L19872	Hs.170087	aryl hydrocarbon receptor		11.3	113	8	3.9
AI471525	Hs.97496	YY1 transcription factor		11.3	124	11	9.7
AA487557	Hs.10706	ESTs; Weakly similar to (defline not available 3882221) [H		11.3	113	8	2.5
M24594	Hs.20315	interferon-induced protein 56		11.2	112	8	5.9
AA279112	Hs.88594	ESTs		11.2	112	1	10.3
AA490969	Hs.168147	ESTs	CQA8	11	187	17	10.4
X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acetyltransferase)		10.8	706	66	9.2
W85765	Hs.30504	ESTs		10.7	123	12	7
AA405569	Hs.418	fibroblast activation protein; alpha	CZA9	10.7	433	41	7.2
N31952	Hs.167531	ESTs; Weakly similar to (defline not available 3875448) [C		10.5	105	4	7.1
H93575	Hs.227146	ESTs		10.5	105	1	9.9
F03969	Hs.16940	ESTs; Weakly similar to tumorous imaginal discs protein T		10.5	105	1	9
N22157	Hs.226573	Homo sapiens IkB kinase-b (IKK-beta) mRNA; complete c		10.5	121	12	1.6
F13673	Hs.99769	ESTs	BCN4	10.4	880	85	5.3
AA131692	Hs.26204	ESTs		10.3	103	1	3.9
AA411745	Hs.239681	ESTs; Weakly similar to KIAA0554 protein [H.sapiens]		10.3	103	1	9.3
D86957	Hs.80712	Human mRNA for KIAA0202 gene; partial cds		10.2	102	1	4.8
AA406542	Hs.71520	ESTs		10.2	506	50	2.8
U65932	Hs.81071	extracellular matrix protein 1	CBC3	10.2	628	62	17.2
AA236813	Hs.72324	ESTs; Highly similar to unknown [H.sapiens]		10.1	111	11	10.2
M90516	Hs.1674	glutamine-fructose-6-phosphate transaminase 1		10	100	1	7.6
AA425309	Hs.33287	nuclear factor I/B	BCQ1	9.9	483	49	1.8
AA487468	Hs.100686	ESTs; Moderately similar to secreted cement gland protei	BCX3	9.9	351	36	13.9
AF007875	Hs.5085	dolichyl-phosphate mannosyltransferase polypeptide 1; ca		9.8	123	13	5
AA398913	Hs.45231	ESTs		9.8	98	1	8.8
HG3748-HT4018		"Basic Transcription Factor, 44 Kda Subunit"		9.7	97	10	7.2
X91868	Hs.54416	sine oculis homeobox (Drosophila) homolog 1		9.7	97	1	9.3
AA599267	Hs.154554	ESTs; Weakly similar to ANKYRIN; BRAIN VARIANT 1 [H		9.7	102	11	6
M23379	Hs.758	RAS p21 protein activator (GTPase activating protein) 1		9.6	96	1	8.5
T25867	Hs.7549	ESTs	BCY9	9.6	124	13	9
U11313	Hs.75760	sterol carrier protein 2		9.5	95	4	8.8
R63542	Hs.110488	ESTs		9.5	95	1	8.5
M69225	Hs.620	bullous pemphigoid antigen 1 (230/240kD)		9.4	94	1	0.3
AA250775	Hs.87747	ESTs		9.4	94	8	7.3
AI039722	Hs.171205	ESTs		9.4	94	3	5.3
U14550	Hs.107573	sialyltransferase		9.3	93	4	3
U18321	Hs.159627	Death associated protein 3		9.3	93	5	8
X89398	Hs.78853	uracil-DNA glycosylase		9.3	93	8	8.2
AA283006	Hs.50758	chromosome-associated polypeptide C		9.3	93	1	8.4
U44378	Hs.75862	MAD (mothers against decapentaplegic; Drosophila) hom		9.3	93	1	7.8
AA187490	Hs.21941	ESTs	AAD1	9.3	436	47	5.8
AA487202	Hs.17962	ESTs		9.2	234	26	16.8
T33637	Hs.6841	ESTs		9.1	91	6	8.3
AA235112	Hs.106227	ESTs; Moderately similar to similar to murine RNA-binding		9.1	91	1	7.6
M83822	Hs.62354	Human beige-like protein (BGL) mRNA; partial cds		9	144	16	13
AA256680	Hs.181104	ESTs		9	117	13	10.6
AA028028	Hs.61460	ESTs	BCX5	9	90	1	5.5
M77142	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protein		8.9	89	5	8
AA858097	Hs.173594	pigment epithelium-derived factor		8.8	110	13	10.5
AA179845	Hs.73625	RAB6 interacting; kinesin-like (rabkinesin6)		8.8	199	23	16.1
AA112396	Hs.44276	ESTs; Moderately similar to HOMEOBOX PROTEIN HOX		8.7	247	29	5.7
U16306	Hs.81800	"Human chondroitin sulfate proteoglycan versican V splice		8.6	568	66	22.4
HG2981-HT3125		"Epican, Alt. Splice 1"		8.5	85	1	3.2
AA280036	Hs.145374	ESTs; Weakly similar to W01A6.c [C.elegans]		8.5	127	15	1.6

FIGURE 10

(CONT.)

D83004	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous to yeast U		8.5	85	1	7.2
AA609200	Hs.162686	ESTs	BCY4	8.5	85	1	4.3
U33147	Hs.46452	mammaglobin 1		8.5	2058	243	1.4
N30856	Hs.30246	ESTs		8.4	84	1	5.3
AA446887	Hs.42911	ESTs		8.4	101	12	8.7
N90526	Hs.54629	ESTs		8.4	84	10	0.8
AA393876	Hs.1255	transcription factor COUP 2 (chicken ovalbumin upstream		8.4	169	20	4.6
AA257971	Hs.21214	ESTs		8.3	83	3	1.8
D60799	Hs.169391	ESTs		8.3	83	8	1.9
AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene h		8.3	87	11	0.4
AA047896	Hs.49169	ESTs		8.3	145	18	3.7
U59863	Hs.146847	TRAF family member-associated NFKB activator		8.2	82	1	6.8
H95094	Hs.75187	KIAA0016 gene product		8.2	124	15	11.5
H13108	Hs.107968	ESTs		8.2	82	1	7.4
AA236324	Hs.92381	ESTs; Weakly similar to !!!! ALU CLASS A WARNING EN	CVA1	8.2	114	14	9.9
L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin; uterine)		8.2	396	48	0.9
T16387	Hs.65328	ESTs		8.2	82	1	6.4
W42451	Hs.92260	high-mobility group protein 2-like 1		8.1	94	12	6.5
Z38501	Hs.8768	ESTs; Weakly similar to neuronal thread protein AD7c-NT		8.1	81	9	5.5
W04517	Hs.18442	ESTs		8.1	81	3	2.8
D31161	Hs.68613	ESTs		8.1	81	1	4.6
AA452000	Hs.94030	ESTs		8.1	101	13	7.9
R40057	Hs.112360	prominin (mouse)-like 1	CZA8	8.1	328	41	1.7
AA451992	Hs.247127	ESTs; Weakly similar to similar to Schizosaccharomyces p		8	84	11	6.3
AA227428	Hs.9728	ESTs; Weakly similar to KIAA0512 protein [H.sapiens]		8	80	6	7.3
AA620599	Hs.24766	ESTs		8	100	13	2.9
N32919	Hs.27931	ESTs		7.9	79	1	6.2
AA398155	Hs.97600	ESTs		7.9	79	1	2.7
R79723	Hs.69997	H.sapiens mRNA for translin associated zinc finger protein		7.9	234	30	18.9
Z29083	Hs.82128	5T4 oncofetal trophoblast glycoprotein	BCA7	7.9	79	2	6.9
AI267886	Hs.148027	polymerase (RNA) II (DNA directed) polypeptide B (140kD		7.8	137	18	11.9
M28213	Hs.78305	RAB2; member RAS oncogene family		7.8	78	1	5.6
R56678	Hs.88959	ESTs; Weakly similar to !!!! ALU SUBFAMILY SP WARNIN		7.7	77	8	6.9
AA031357	Hs.31803	ESTs		7.7	77	1	5.1
N66857	Hs.14808	ESTs; Weakly similar to !!!! ALU CLASS C WARNING EN		7.7	77	1	5
Z39436	Hs.102720	ESTs		7.7	81	11	7.6
T90037	Hs.16686	ESTs		7.6	76	1	4.2
AA167268	Hs.62349	ESTs		7.6	92	12	1.4
R34531	Hs.243068	KIAA0480 gene product		7.6	76	1	5
AA416997	Hs.59622	ESTs		7.6	144	19	13.9
AA211400	Hs.193172	ESTs		7.5	112	15	2.5
D60237	Hs.14368	SH3-binding domain glutamic acid-rich protein like		7.5	75	1	6.5
W37145	Hs.30029	ESTs	PAA9	7.5	136	18	3.4
AA054228	Hs.23165	ESTs		7.4	74	1	6
AA455875	Hs.227602	Homo sapiens mRNA for KIAA0727 protein; partial cds		7.4	74	3	1.7
AA043562	Hs.62637	ESTs		7.4	74	8	6
D62657	Hs.35086	ubiquitin-specific protease 1		7.4	103	14	6.5
AA044842	Hs.95260	ESTs		7.4	74	5	2.4
AA159181	Hs.184013	ESTs		7.4	137	19	1.8
M99701	Hs.95243	transcription elongation factor A (SII)-like 1		7.3	73	1	5.3
Z46629	Hs.2316	SRY (sex-determining region Y)-box 9 (campomelic dyspl		7.3	73	1	5.2
AA165333	Hs.24808	ESTs		7.3	73	1	3.8
N90719	Hs.94445	ESTs		7.3	73	3	5.4
L38608	Hs.10247	activated leucocyte cell adhesion molecule		7.3	106	15	5
R87834	Hs.3688	acid-inducible phosphoprotein		7.3	73	1	1.2
AA042990	Hs.171921	sema domain; immunoglobulin domain (Ig); short basic do		7.3	271	37	2.3
N64378	Hs.13149	ESTs; Weakly similar to ARI protein [D.melanogaster]		7.2	72	10	6.1
AA478446	Hs.69559	ESTs; Weakly similar to Bat2 [H.sapiens]		7.2	72	1	5.7
U83908	Hs.247134	Homo sapiens nuclear antigen H731-like protein mRNA; c		7.2	72	1	5.8
W60913	Hs.30738	ESTs		7.2	72	4	5.7

FIGURE 10
(CONT.)

AA393164	Hs.97644	mammaglobin 2	7.2	498	69	9.3
F10577	Hs.70312	ESTs; Moderately similar to neuronal thread protein AD7c	7.1	71	9	6.9
AA211941	Hs.109643	polyadenylate binding protein-interacting protein 1	7.1	71	1	6.2
X57985	Hs.2178	H2B histone family; member Q	7.1	100	14	7.5
M57230	Hs.82065	interleukin 6 signal transducer (gp130; oncostatin M recep	7.1	71	4	6.4
D61676	Hs.21851	Homo sapiens mRNA; cDNA DKFZp586J2118 (from clone BCB9	7.1	392	56	3.6
H18027	Hs.184697	receptor for virally-encoded semaphorin BCY7	7.1	150	21	14.5
AA199828	Hs.188662	ESTs BCY8	7.1	71	1	6.5
AA032147	Hs.23296	ESTs	7	70	1	6.5
AA436244	Hs.17240	ESTs	7	70	3	1.3
AA400080	Hs.97774	EST	7	70	1	0.9
U25435	Hs.57419	transcriptional repressor	7	115	17	5.4
M74524	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	7	97	14	7.5
W47183	Hs.153468	ESTs; Weakly similar to !!!! ALU SUBFAMILY SB2 WARN	7	70	6	6
M60752	Hs.121017	H2A histone family; member A	6.9	103	15	8.4
J03460	Hs.99949	prolactin-induced protein	6.9	1494	218	1.3
AA292701	Hs.5364	ESTs	6.9	69	1	4.4
AA219699	Hs.184245	ESTs	6.9	69	5	6.2
H64938	Hs.38331	ESTs	6.9	69	10	2.4
Z38839	Hs.125019	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING	6.9	319	47	2.1
W86779	Hs.241582	EST	6.9	162	24	2.6
AA261852	Hs.192905	ESTs	6.8	68	1	0.2
AI283493	Hs.75722	ribophorin II	6.8	223	33	2.8
H17861	Hs.17767	ESTs	6.8	129	19	12.1
J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	6.8	68	1	5.6
AA608955	Hs.109653	ESTs	6.8	68	10	6.1
U39840	Hs.105440	hepatocyte nuclear factor 3; alpha	6.7	67	9	6.3
AA425367	Hs.32094	ESTs	6.7	94	14	8
H48502	Hs.28212	ESTs	6.7	78	12	3
Z38763	Hs.15740	ESTs	6.7	67	1	6.3
AA598803	Hs.111496	ESTs	6.7	67	2	2.1
AI287461	Hs.164950	ESTs	6.7	67	1	6
N45219	Hs.48320	ESTs	6.7	155	23	1.4
AA195260	Hs.204151	ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WAR	6.7	67	1	5.7
F09012	Hs.181326	ESTs	6.7	67	6	1.9
L11066	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	6.7	93	14	8.4
AA453783	Hs.76550	ESTs; Weakly similar to unknown [H.sapiens]	6.7	304	46	7.8
T25508	Hs.81057	ESTs	6.7	67	9	5.7
L40391	Hs.6445	Homo sapiens (clone s153) mRNA fragment	6.6	135	21	13.1
AA147719	Hs.159441	ESTs	6.6	66	1	5.4
AA126433	Hs.173242	sorting nexin 4	6.6	69	11	6.3
M21305	Hs.247946	Human alpha satellite and satellite 3 junction DNA sequen	6.5	878	135	0.8
AA041551	Hs.48644	ESTs	6.5	65	2	6
R42036	Hs.6763	ESTs	6.5	65	10	1.5
T40530	Hs.231577	ESTs	6.5	65	6	4.8
N29888	Hs.169539	ESTs	6.5	65	4	5.3
AA490862	Hs.55901	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WA	6.5	65	1	5.6
R99599	Hs.103804	heterogeneous nuclear ribonucleoprotein U (scaffold attac	6.5	162	25	14.7
M63256	Hs.75124	cerebellar degeneration-related protein (62kD)	6.4	64	2	4.9
U37519	Hs.87539	aldehyde dehydrogenase 8	6.4	428	67	2.3
AB002367	Hs.21355	doublecortin and CaM kinase-like 1	6.4	64	8	3
AA284755	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	6.4	64	8	6
AA243012	Hs.75928	ESTs	6.4	67	11	5
AI356250	Hs.4779	ESTs	6.4	74	12	6.6
X06700	Hs.119571	collagen; type III; alpha 1 (Ehlers-Danlos syndrome type I	6.4	1111	175	5
U51166	Hs.173824	thymine-DNA glycosylase	6.4	100	16	4.4
W23625	Hs.8739	ESTs	6.4	64	1	5.1
M15796	Hs.78996	proliferating cell nuclear antigen	6.4	249	39	22.4
HG4390-HT4660		Ribosomal Protein L18a Homolog	6.3	63	4	5.7
X92098	Hs.75914	H.sapiens mRNA for transmembrane protein rnp24	6.3	98	16	9.1

FIGURE 10
(CONT.)

N67711	Hs.151046	Homo sapiens clone 23859 mRNA sequence		6.3	63	1	5.8
W37999	Hs.24336	ESTs		6.3	63	6	5
AA149894	Hs.20815	erythroblast macrophage protein		6.3	165	26	3.2
H10933	Hs.10067	ESTs	BCA1	6.3	693	110	7.2
AA609723	Hs.30652	ESTs	PAA3	6.3	63	1	5.4
AA122386	Hs.82985	collagen; type V; alpha 2		6.3	1075	171	3.8
AA243052	Hs.172643	Homo sapiens mRNA; cDNA DKFZp564J1616 (from clone		6.2	62	6	5.6
R39995	Hs.25925	Homo sapiens clone 23860 mRNA sequence		6.2	62	2	5.9
AA430124	Hs.234607	ESTs		6.2	62	1	5.4
T68510	Hs.76704	ESTs		6.2	600	97	4.1
R79750	Hs.83623	constitutive androstane receptor-beta; orphan nuclear hor		6.1	493	81	0.7
U35835	Hs.155637	protein kinase; DNA-activated; catalytic polypeptide		6.1	61	1	5.7
AA046405	Hs.5306	ESTs; Weakly similar to KIAA0597 protein [H.sapiens]		6.1	61	2	5.9
AA358268	Hs.95464	ESTs; Moderately similar to transcription factor RTEF-1 [H		6.1	61	1	5.1
D31058	Hs.24375	ESTs	CXA3	6.1	343	56	16.4
U70322	Hs.168075	karyopherin (importin) beta 2		6.1	126	21	2.4
R46025	Hs.7413	ESTs		6.1	185	31	6.6
W68845	Hs.24095	ESTs		6.1	110	18	10.2
AA176690	Hs.4084	ESTs		6	60	6	4.6
N67390	Hs.43228	ESTs		6	60	5	3.7
L09717	Hs.8262	lysosomal-associated membrane protein 2		6	60	5	5.9
F03819	Hs.173094	ESTs		6	202	34	3.7
D38491	Hs.247463	Human mRNA for KIAA0117 gene; partial cds		5.9	59	1	2.6
F02582	Hs.14474	ESTs		5.9	59	10	4.2
AA347193	Hs.62180	ESTs		5.9	59	1	4.2
AA504642	Hs.28436	ESTs; Weakly similar to coded for by C. elegans cDNA CE		5.9	59	1	4.4
AA476594	Hs.9817	arg/Abl-interacting protein ArgBP2		5.9	186	32	3.7
Z81326	Hs.78589	protease inhibitor 12 (neuroserpin)		5.9	59	1	3.3
F10707	Hs.181104	ESTs		5.9	208	36	1.8
X07696	Hs.80342	keratin 15		5.8	753	131	0.4
X53793	Hs.117950	multifunctional polypeptide similar to SAICAR synthetase		5.8	218	38	13
AB000221	Hs.16530	small inducible cytokine subfamily A (Cys-Cys); member 1		5.8	58	1	3.2
AA458904	Hs.26267	ESTs; Weakly similar to torsinA [H.sapiens]		5.8	58	5	3.1
W63793	Hs.75744	S-adenosylmethionine decarboxylase 1		5.8	151	26	11.4
AA262491	Hs.186572	ESTs		5.8	58	1	5
AA429038	Hs.40541	ESTs		5.8	58	1	4.4
AA608531	Hs.170313	ESTs		5.8	58	1	4.9
L19161	Hs.211539	eukaryotic translation initiation factor 2; subunit 3 (gamma		5.8	171	30	2.9
R27296	Hs.23240	ESTs		5.8	115	20	2.5
AA610086	Hs.32990	ESTs		5.8	91	16	1.4
D87685	Hs.78893	Human mRNA for KIAA0244 gene; partial cds		5.8	58	1	4.9
AA262943	Hs.23552	ESTs	BCH5	5.8	336	58	2
D60302	Hs.108977	ESTs	BCY1	5.8	321	55	17
AA194882	Hs.19522	ESTs		5.7	57	8	5.3
AA287097	Hs.244443	transcription factor 4		5.7	57	8	4.1
AA463745	Hs.29403	ESTs; Weakly similar to PROBABLE ATP-DEPENDENT R		5.7	57	10	4.8
AA490814	Hs.24170	ESTs		5.7	94	17	7.3
AA084677	Hs.54558	ESTs; Weakly similar to !!!! ALU CLASS C WARNING EN		5.7	57	1	4.9
Z39301	Hs.7859	ESTs		5.7	57	1	4.9
AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis; secreted cement glan		5.7	368	65	28.5
AA044095	Hs.3402	ESTs		5.7	57	1	4.5
AA092376	Hs.90606	15 kDa selenoprotein		5.7	57	1	5
R51309	Hs.70823	KIAA1077 protein	BCN5	5.7	567	100	6.7
X16396	Hs.154672	methylene tetrahydrofolate dehydrogenase (NAD+ depen		5.7	251	44	6.6
AA024835	Hs.47584	potassium voltage-gated channel; delayed-rectifier; subfa		5.7	85	15	7.8
D87448	Hs.91417	Homo sapiens mRNA for DNA topoisomerase II binding p		5.6	76	14	2
U90914	Hs.5057	carboxypeptidase D		5.6	56	1	5.3
X72841	Hs.31314	H.sapiens IEF 7442 mRNA		5.6	191	34	3.5
AA281591	Hs.16193	Homo sapiens mRNA; cDNA DKFZp586B211 (from clone		5.6	101	18	1.6
AA464428	Hs.119394	ESTs		5.6	108	20	1.8

FIGURE 10
(CONT.)

AA280617	Hs.100861	ESTs; Weakly similar to p60 katanin [H.sapiens]		5.6	73	13	6.1
X52003	Hs.1406	trefoil factor 1 (breast cancer; estrogen-inducible sequenc	BCO7	5.6	1346	239	5.4
AA121266	Hs.34641	ESTs	PAA8	5.6	95	17	9.1
AA521472	Hs.73435	ESTs		5.6	106	19	9
D87469	Hs.57652	EGF-like-domain; multiple 2		5.5	145	27	2.2
AA452411	Hs.29679	ESTs		5.5	147	27	4.4
AA504631	Hs.26813	ESTs; Weakly similar to (defline not available 4689108) [H		5.5	130	24	12.5
AA621557	Hs.58633	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WA		5.5	315	58	3.1
AI051602	Hs.4112	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coen		5.5	55	10	4.2
AA418069	Hs.241391	natural killer-tumor recognition sequence		5.5	63	12	1
T26989	Hs.121576	aspartate beta-hydroxylase		5.5	79	15	4.4
AA143019	Hs.182667	ESTs; Highly similar to surface 4 integral membrane prote		5.5	90	17	2.9
W90146	Hs.35962	ESTs		5.5	168	31	4.4
N37065	Hs.44856	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WA		5.5	323	59	10.5
T23983	Hs.7365	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WA		5.5	186	34	16.5
AA130273	Hs.7584	ESTs; Weakly similar to (defline not available 4240269) [H	BCF3	5.5	55	1	5.2
AA262942	Hs.79741	ESTs		5.5	343	62	2.5
M86546	Hs.155691	pre-B-cell leukemia transcription factor 1		5.4	180	34	15.9
U15932	Hs.2128	dual specificity phosphatase 5		5.4	137	26	2.5
AA338760	Hs.15159	ESTs		5.4	54	1	4.4
AA460350	Hs.22370	ESTs		5.4	75	14	0.8
AA133250	Hs.62180	ESTs		5.4	54	1	4
N22414		"yw39a07.s1 Weizmann Olfactory Epithelium Homo sapie		5.4	54	1	3.7
N63823	Hs.220470	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WA		5.4	54	1	4.3
W60473	Hs.57787	ESTs		5.4	54	1	4.1
AA287115	Hs.99697	ESTs		5.4	54	10	2.5
AA313639	Hs.185783	ESTs		5.4	73	14	6.8
M14219	Hs.76152	decorin		5.4	144	27	13.3
N79749	Hs.87627	ESTs		5.4	81	15	2.6
H89575	Hs.93468	ESTs		5.4	259	48	1.4
D59894	Hs.34782	ESTs	BCJ1	5.4	483	90	4
AA485223	Hs.34892	ESTs		5.4	192	36	4.4
U43189	Hs.82143	Human Ets transcription factors NERF-1a and NERF-1b (		5.3	53	1	4.8
AA347973	Hs.221132	ESTs		5.3	67	13	5.3
AA459657	Hs.12311	Homo sapiens clone 23570 mRNA sequence		5.3	166	32	14.9
AA130596	Hs.71331	ESTs; Weakly similar to potent heat-stable protein phosph		5.3	53	1	2.8
R45175	Hs.117183	ESTs		5.3	53	6	2.3
Z39549	Hs.153746	ESTs		5.3	53	5	0.9
AA292655	Hs.96557	ESTs		5.3	58	11	3.3
F02641	Hs.12342	Homo sapiens clone 24538 mRNA sequence		5.3	53	9	3.6
AA610070	Hs.151469	ESTs; Highly similar to CASK [H.sapiens]		5.3	53	9	3.2
W52493	Hs.13531	ESTs		5.3	53	1	4.1
H46617	Hs.172241	"yp19h1.r1 Soares breast 3NbHBst Homo sapiens cDNA	CVA3	5.3	144	27	13.1
AA449887		ESTs		5.2	52	1	4.3
AA101416	Hs.107149	ESTs		5.2	52	3	2.3
AA406546	Hs.71968	ESTs		5.2	405	78	10.1
AA465701	Hs.108646	ESTs		5.2	52	4	3.9
W80702	Hs.58461	ESTs		5.2	52	6	1.8
AA837495	Hs.69851	ESTs; Weakly similar to Wiskott-Aldrich syndrome protein		5.2	81	16	1.1
AA090695	Hs.181385	ESTs		5.2	75	15	6.4
AA132007	Hs.167420	ESTs		5.2	251	48	21
Y00503	Hs.182265	keratin 19		5.2	1320	256	3.2
AA418230	Hs.8172	ESTs; Weakly similar to alternatively spliced product using		5.2	52	1	4.9
M22995	Hs.865	RAP1A; member of RAS oncogene family		5.2	52	1	3
U89326	Hs.87223	bone morphogenetic protein receptor; type IB		5.2	52	5	3.5
X63629	Hs.2877	cadherin 3; P-cadherin (placental)		5.2	331	64	1.5
AA122147	Hs.64691	Homo sapiens mRNA for KIAA0483 protein; partial cds		5.2	117	23	5
D14878	Hs.82043	D123 gene product		5.1	106	21	9.2
AA236559	Hs.8768	ESTs; Weakly similar to neuronal thread protein AD7c-NT		5.1	181	36	15.8
AA598710	Hs.23740	ESTs		5.1	298	59	4.4

FIGURE 10
(CONT.)

AA252863	Hs.87729	ESTs		5.1	51	1	4.2
AA456099	Hs.176376	ESTs		5.1	51	1	2
AA479362	Hs.47144	ESTs		5.1	198	39	17.9
AA398302	Hs.127437	ESTs		5.1	51	1	2.4
W68502	Hs.180201	ESTs; Weakly similar to !!!! ALU CLASS C WARNING EN		5.1	58	12	5.7
R51273	Hs.79029	ESTs		5.1	51	9	3.8
N46086	Hs.92308	ESTs		5.1	150	30	7.2
N33236	Hs.28555	ESTs	BCO1	5.1	51	1	3.9
M22898	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)		5.1	97	19	9.3
W44735	Hs.9286	ESTs		5.1	51	5	4.5
Z39053	Hs.27263	ESTs		5.1	113	22	6.1
U67319	Hs.9216	caspase 7; apoptosis-related cysteine protease		5	66	13	5.3
AA004415	Hs.106106	ESTs		5	468	94	4.7
F10770	Hs.180378	Homo sapiens clone 669 unknown mRNA; complete sequ		5	50	5	4.1
N26101	Hs.7838	ESTs		5	50	1	4.3
N36421	Hs.107854	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WA		5	50	1	4.7
N57773	Hs.93560	ESTs; Weakly similar to Similar to Rat trg gene product [C		5	50	2	3.1
N93839	Hs.39288	ESTs; Weakly similar to !!!! ALU SUBFAMILY SB WARNIN		5	50	5	4.7
AA608679	Hs.108327	damage-specific DNA binding protein 1 (127kD)		5	121	25	5.9
AI382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein		5	285	58	1.2
W78968	Hs.241880	H3 histone; family 3A		5	264	53	3.4
AA129465	Hs.106843	ESTs; Weakly similar to hypothetical protein [H.sapiens]		5	50	1	3.3
H88033	Hs.109727	Homo sapiens mRNA for KIAA0733 protein; partial cds		5	64	13	6.3
U84573	Hs.41270	procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine h		5	225	45	9.1
N59764	Hs.5398	GUANINE-MONOPHOSPHATE SYNTHETASE		5	50	1	4.1
H06195	Hs.7194	ESTs		5	110	22	9.7
U47414	Hs.79069	cyclin G2		5	50	1	3.2
HG3510-HT3704		V-Erba Related Ear-3 Protein		5	82	17	0.9
U24576		LIM domain only 4		4.9	49	1	3.6
X65724	Hs.2839	Norrie disease (pseudoglioma)		4.9	49	5	3.8
X98263	Hs.152720	M-phase phosphoprotein 6		4.9	153	31	2.4
AA315807	Hs.106227	ESTs; Weakly similar to (defline not available 4200325) [H		4.9	49	1	4.2
AA348014	Hs.23412	ESTs		4.9	49	1	4.5
AA446949	Hs.6236	ESTs		4.9	337	70	2.7
AA456981	Hs.35349	ESTs		4.9	49	1	4.1
AA193592	Hs.42300	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WA		4.9	121	25	10.4
H28581	Hs.92711	ESTs		4.9	108	22	9
N51056	Hs.38891	ESTs		4.9	49	1	4.4
AA430487	Hs.95424	ESTs		4.9	49	7	3.7
AA442868	Hs.13531	ESTs; Weakly similar to (defline not available 5081652) [H		4.9	68	14	1.4
AA435633	Hs.18879	Homo sapiens clone 23965 mRNA sequence		4.9	49	1	4.3
R55185	Hs.3321	ESTs; Highly similar to iroquois-class homeodomain prote		4.9	632	129	1.7
AA257056	Hs.7972	Homo sapiens mRNA for KIAA0871 protein; complete cds		4.9	49	1	4.1
AA455917	Hs.50785	SEC22; vesicle trafficking protein (S. cerevisiae)-like 1		4.9	49	1	4.4
AA329274	Hs.82911	protein tyrosine phosphatase type IVA; member 2		4.9	163	34	15.1
D87969	Hs.82921	CMP-sialic acid transporter		4.9	49	3	3.8
AA451712	Hs.171581	ESTs		4.9	49	1	3.7
X99585	Hs.180139	H.sapiens mRNA for SMT3B protein		4.9	261	53	3.7
M21389	Hs.195850	keratin 5 (epidermolysis bullosa simplex; Dowling-Meara/K		4.8	622	130	0.7
AA001049	Hs.24713	ESTs		4.8	231	49	7.3
AA280670	Hs.24968	ESTs		4.8	79	17	5.2
AA398533	Hs.22209	ESTs		4.8	134	28	3.2
D51095	Hs.35861	ESTs		4.8	48	8	3.1
AA132983	Hs.44155	ESTs; Moderately similar to C-1-TETRAHYDROFOLATE		4.8	96	20	6.5
N69514	Hs.28877	ESTs; Weakly similar to predicted using Genefinder [C.ele		4.8	61	13	5.6
R73468	Hs.140996	ESTs		4.8	48	2	3.4
AA258030	Hs.55356	ESTs; Weakly similar to (defline not available 3874821) [C		4.8	48	1	4.4
AA489046	Hs.94109	ESTs		4.8	179	38	2.8
H88261	Hs.130093	ESTs		4.8	48	1	2.5
H97225	Hs.38592	ESTs		4.8	48	1	0.9

FIGURE 10
(CONT.)

AA236010	Hs.26613	ESTs		4.8	48	1	0.5
AA748483	Hs.191356	Homo sapiens basic transcription factor 2 p44 (btf2p44) g		4.8	48	5	4.1
AA412108	Hs.191803	ESTs		4.8	106	22	1
AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal chondrody		4.8	312	65	30.9
X74987	Hs.12013	ribonuclease L (2';5'-oligoisoadenylate synthetase-depend		4.8	48	8	3.8
AA609427	Hs.210706	ESTs; Moderately similar to !!!! ALU SUBFAMILY SP WAR		4.8	48	1	4.1
AA459555	Hs.31921	Homo sapiens mRNA for KIAA0648 protein; partial cds		4.8	48	1	4.6
W79865	Hs.58367	glypican 4		4.8	48	1	3.6
X06323	Hs.79086	Human MRL3 mRNA for ribosomal protein L3 homologue		4.8	246	51	3.9
AA165231	Hs.8184	ESTs		4.8	53	11	3.7
R38185	Hs.83954	ESTs; Moderately similar to (defline not available 4335943		4.8	153	32	4.3
AA129390	Hs.5285	ESTs	CQA1	4.8	93	20	3.1
D14661	Hs.119	gene predicted from cDNA with a complete coding sequen		4.7	119	26	3
D25538	Hs.172199	adenylate cyclase 7		4.7	47	1	4.3
D26361	Hs.3104	KIAA0042 gene product		4.7	47	4	0.7
HG4557-HT4962		"Small Nuclear Ribonucleoprotein U1, 1snrp"		4.7	47	1	4.2
C02582	Hs.109253	ESTs; Highly similar to (defline not available 5114045) [H.		4.7	229	49	7.9
AA040154	Hs.32478	ESTs		4.7	201	43	4.5
AA286809	Hs.28423	ESTs		4.7	152	33	5.3
AA412473	Hs.25880	ESTs		4.7	47	1	4
AA026894	Hs.42826	ESTs; Weakly similar to !!!! ALU CLASS B WARNING EN		4.7	47	4	4.3
N24716	Hs.12244	ESTs		4.7	47	4	4.2
R68425	Hs.28886	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WA		4.7	54	12	4.5
AA055768	Hs.122576	ESTs		4.7	770	166	5.8
AA165313	Hs.131189	ESTs		4.7	57	12	4.7
AA478625		ESTs		4.7	59	13	4.7
AA044840	Hs.241676	stromal cell-derived factor 1		4.7	114	25	0.9
N90960	Hs.227459	ESTs; Moderately similar to !!!! ALU SUBFAMILY SP WAR		4.7	151	32	9.3
AA873285	Hs.137947	ESTs		4.7	47	3	4.4
D21262	Hs.75337	Human mRNA for KIAA0035 gene; partial cds		4.7	47	1	4
AA214305	Hs.76173	ESTs		4.7	47	1	4.1
AA235803	Hs.9946	ESTs		4.7	710	151	2.5
AA102520	Hs.168017	ESTs; Weakly similar to heat shock protein hsp40 homolo	BCH2	4.7	556	119	4.5
AA491465	Hs.28792	ESTs	BCU9	4.7	381	81	6.4
AA393803	Hs.16869	ESTs		4.7	747	158	5.7
U02680	Hs.82643	protein tyrosine kinase 9		4.6	148	32	11.3
U18291	Hs.1592	CDC16 (cell division cycle 16; S. cerevisiae; homolog)		4.6	151	33	2
AA476473	Hs.247244	Homo sapiens Trio mRNA; complete cds		4.6	46	1	4
AA609943	Hs.32793	ESTs		4.6	71	16	3.6
T34527	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acet		4.6	199	44	19.2
W19222	Hs.7041	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNI		4.6	46	4	4.3
AA400247	Hs.42173	ESTs		4.6	46	2	1.8
H29532	Hs.101174	microtubule-associated protein tau		4.6	163	35	7.3
N49408	Hs.136102	Homo sapiens mRNA for KIAA0853 protein; partial cds		4.6	46	1	3.8
W02102	Hs.53565	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING		4.6	60	13	4.8
W69134	Hs.57987	ESTs		4.6	46	7	0.8
AA412488	Hs.48820	ESTs		4.6	46	3	0.8
AA447504	Hs.100261	ESTs		4.6	46	8	3.9
AA437118	Hs.11500	ESTs		4.6	199	44	2.3
AA421139	Hs.173542	ESTs		4.6	239	53	3.5
N64405	Hs.29379	ESTs		4.6	46	7	3.8
AA431459	Hs.47783	ESTs		4.6	46	1	4.3
AA447230	Hs.5070	ESTs		4.6	46	1	4.4
AA135468	Hs.71573	ESTs		4.6	46	5	3.5
R38102	Hs.50421	KIAA0203 gene product		4.6	69	15	5.8
J04177	Hs.82772	collagen; type XI; alpha 1	BCA8	4.6	1216	267	4.4
H25577	Hs.176588	ESTs; Weakly similar to (defline not available 4519535) [H	BCB1	4.6	913	199	2.9
AA047036	Hs.62817	ESTs	BCR9	4.6	427	93	10.4
AA148885	Hs.154443	minichromosome maintenance deficient (S. cerevisiae) 4		4.6	196	43	10
AA190993	Hs.246174	a disintegrin and metalloproteinase domain 12 (meltrin alp		4.6	132	29	9.7

FIGURE 10
(CONT.)

D37965	Hs.170040	platelet-derived growth factor receptor-like		4.5	45	4	4
U33052	Hs.69171	protein kinase C-like 2		4.5	45	1	3.6
U71207	Hs.29279	eyes absent (Drosophila) homolog 2		4.5	45	1	2.8
AA195399	Hs.24641	ESTs		4.5	45	1	3.6
AA233168	Hs.3585	ESTs; Weakly similar to coded for by C. elegans cDNA CE		4.5	45	10	0.5
AA281623	Hs.7525	ESTs; Weakly similar to (defline not available 3882205) [H		4.5	45	1	3.7
AA435542	Hs.25796	ESTs		4.5	116	26	4.5
AA489790	Hs.167496	Homo sapiens Ran-GTP binding protein mRNA; partial cd		4.5	45	1	3.8
AA036811	Hs.165030	ESTs		4.5	45	1	3.8
W94942	Hs.177534	ESTs; Weakly similar to dual-specificity protein tyrosine ph		4.5	45	4	2.6
Z40861	Hs.6540	ESTs		4.5	45	2	3
AA253217	Hs.41271	ESTs		4.5	290	65	3.7
AA279943	Hs.122579	ESTs		4.5	96	21	7.8
AA459956	Hs.49163	ESTs		4.5	45	9	3.4
F04816	Hs.92127	ESTs		4.5	96	22	6.9
N39214	Hs.44708	ser-Thr protein kinase related to the myotonic dystrophy p		4.5	211	47	5
AA621785	Hs.170008	ESTs		4.5	45	2	3.6
X56199	Hs.244401	constitutive androstane receptor-beta; orphan nuclear hor		4.5	45	1	2.4
Z38919	Hs.21929	ESTs		4.5	45	1	2.5
AA430008	Hs.8117	ESTs		4.5	137	31	12
D38073	Hs.179565	minichromosome maintenance deficient (S. cerevisiae) 3		4.5	45	2	3.4
U41060	Hs.79136	Human breast cancer; estrogen regulated LIV-1 protein (L	BCR4	4.5	1472	330	2.1
D78611	Hs.79284	mesoderm specific transcript (mouse) homolog	CBC1	4.5	129	29	3.1
T17185	Hs.4299	ESTs	CHA1	4.5	390	87	5.3
U85658	Hs.61796	transcription factor AP-2 gamma (activating enhancer-bind		4.4	255	58	1.6
AA412059	Hs.26864	ESTs		4.4	174	40	1.6
AA452590	Hs.30348	ESTs		4.4	222	51	1.8
AA464708	Hs.249247	ESTs; Weakly similar to alternatively spliced product using		4.4	371	84	3.2
AA009528	Hs.42743	ESTs; Weakly similar to predicted using Genefinder [C.ele		4.4	73	17	6.2
H97678	Hs.31319	ESTs		4.4	103	24	3.8
W92713	Hs.11732	ESTs		4.4	44	6	2.3
Z39211	Hs.150926	fucose-1-phosphate guanylyltransferase		4.4	104	24	5.1
AA024604	Hs.26102	ESTs		4.4	44	1	3
AA401474	Hs.208414	ESTs		4.4	44	7	1.1
W72967	Hs.191381	ESTs		4.4	44	1	3.1
AA425887	Hs.98502	ESTs		4.4	48	11	0.9
AI334393	Hs.18113	ESTs		4.4	76	18	1
N59212	Hs.236081	C-terminal binding protein 2		4.4	44	1	3.8
L07493	Hs.1608	replication protein A3 (14kD)		4.4	44	1	4.1
AA281770	Hs.184081	seven in absentia (Drosophila) homolog 1		4.4	53	12	2.1
X54199	Hs.82285	phosphoribosylglycinamide formyltransferase; phosphorib		4.4	44	1	4.1
X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glutamate gamma-sem		4.3	77	18	7.2
AA226968	Hs.22826	ESTs		4.3	43	1	3.9
AA398892	Hs.24391	ESTs		4.3	772	179	1.7
AA399414	Hs.28332	ESTs		4.3	43	1	3.7
AA465093	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protein		4.3	101	24	1.6
AA489636	Hs.25253	ESTs		4.3	43	10	2.2
AA025728	Hs.61307	ESTs		4.3	43	10	2.7
N59543	Hs.15456	PDZ domain containing 1		4.3	43	1	2
N69113	Hs.110855	ESTs		4.3	43	1	1
N89820	Hs.14559	ESTs		4.3	43	5	2.2
R53439	Hs.194149	ESTs		4.3	45	11	4.4
W60439	Hs.119370	ESTs; Moderately similar to cbp146 [M.musculus]		4.3	43	8	3.6
W81552	Hs.242943	constitutive androstane receptor-beta; orphan nuclear hor		4.3	819	191	1.2
N79820	Hs.50854	ESTs		4.3	162	38	12.1
T79274	Hs.10175	ESTs		4.3	65	15	5.7
Z36290	Hs.173933	ESTs; Weakly similar to NUCLEAR FACTOR 1/X [H.sapie		4.3	43	1	3.5
R25607	Hs.23978	scaffold attachment factor B		4.3	68	16	2.8
AA916752	Hs.244697	ESTs; Highly similar to MEM3 [M.musculus]		4.3	152	35	12.5
N79516	Hs.73287	ESTs		4.3	43	1	3.9

FIGURE 10
(CONT.)

F13665	Hs.65641	ESTs		4.3	190	44	5.4
AB003103	Hs.4295	proteasome (prosome; macropain) 26S subunit; non-ATP		4.2	152	36	12.2
L37936	Hs.3273	Ts translation elongation factor; mitochondrial		4.2	50	12	4.4
U14518	Hs.1594	centromere protein A (17kD)		4.2	42	7	3.4
U90919	Hs.7137	Human clones 23667 and 23775 zinc finger protein mRNA		4.2	42	7	3.7
AA058846	Hs.33363	ESTs		4.2	135	32	4
AA171736	Hs.35947	ESTs; Highly similar to methyl-CpG binding protein MBD4		4.2	90	22	2.8
AA227145	Hs.209473	ESTs; Moderately similar to transformation-related protein		4.2	56	14	2.2
H08778	Hs.133521	ESTs		4.2	58	14	0.8
R40576	Hs.21590	ESTs; Weakly similar to !!!! ALU SUBFAMILY SC WARNIN		4.2	125	30	7.4
R66534	Hs.28403	ESTs		4.2	42	6	3.6
Z39898	Hs.21948	ESTs		4.2	46	11	1.4
AA251524	Hs.44649	ESTs		4.2	42	9	1.1
F08813	Hs.97413	ret finger protein-like 3 antisense		4.2	42	1	2.7
AA191353	Hs.22385	ESTs		4.2	124	30	1.8
AA412494	Hs.98152	ESTs		4.2	77	19	1.4
AA599786	Hs.112110	ESTs		4.2	42	7	2.9
R01073	Hs.191202	ESTs		4.2	42	7	3
AA504343	Hs.183475	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARN		4.2	104	25	7.8
N30436	Hs.11556	ESTs		4.2	42	1	3.8
U38847	Hs.151518	TAR (HIV) RNA-binding protein 1		4.2	46	11	1.1
AA608856	Hs.431	murine leukemia viral (bmi-1) oncogene homolog		4.2	42	1	2.2
W85888	Hs.47334	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WA		4.2	159	38	7.1
AA453614	Hs.5460	Homo sapiens mRNA for KIAA0776 protein; partial cds		4.2	171	41	12.6
X57025	Hs.85112	insulin-like growth factor 1 (somatomedin C)		4.2	42	5	2.6
D63391	Hs.6793	platelet-activating factor acetylhydrolase; isoform Ib; gamm		4.2	187	44	5.4
AA427861	Hs.59503	ESTs		4.2	79	19	1.9
D14657	Hs.81892	KIAA0101 gene product		4.1	320	78	10.6
D29677	Hs.3085	KIAA0054 gene product		4.1	64	16	3
HG2755-HT2862		T-Plastin		4.1	259	63	1.9
L05425		Homo sapiens autoantigen mRNA; complete cds		4.1	53	13	4
U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatidate cytidylyltrans		4.1	41	1	3.3
U79293	Hs.159264	Human clone 23948 mRNA sequence		4.1	41	1	2.4
X75042	Hs.44313	v-rel avian reticuloendotheliosis viral oncogene homolog		4.1	53	13	4.9
AA236950	Hs.8115	ESTs		4.1	41	2	3.3
H06746	Hs.20072	ESTs		4.1	41	7	1.7
N90430	Hs.6616	ESTs		4.1	41	1	2.6
AA436475	Hs.190104	ESTs		4.1	43	11	1.6
D82808	Hs.17820	Rho-associated; coiled-coil containing protein kinase 1		4.1	41	1	3.6
N77151	Hs.61638	Homo sapiens mRNA for KIAA0799 protein; partial cds		4.1	62	15	4.9
AA093348	Hs.7306	secreted frizzled-related protein 1		4.1	374	91	1.1
W95070	Hs.74316	desmoplakin (DPI; DPII)		4.1	640	158	3
AA243746	Hs.211577	ESTs; Highly similar to CG1 protein [H.sapiens]		4.1	301	73	6.1
AA169379	Hs.72865	ESTs	BCU4	4.1	334	82	3.4
AA490890	Hs.105273	ESTs		4.1	72	18	1.5
D86961	Hs.79299	lipoma HMGIC fusion partner-like 2		4	40	1	3.8
L28997	Hs.77102	ADP-ribosylation factor-like 1		4	110	28	10.7
AA281245	Hs.23317	ESTs		4	75	19	1.7
AA393793	Hs.110347	ESTs; Highly similar to (defline not available 4468913) [H.		4	40	3	3.2
AA171755	Hs.181915	ESTs		4	40	7	1.1
R51818	Hs.104222	ESTs		4	70	18	6.8
W72471	Hs.23920	ESTs		4	48	12	4
T23820	Hs.155478	cyclin T2		4	40	4	1.2
T56679	Hs.865	RAP1A; member of RAS oncogene family		4	40	1	3.4
H03686	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding prote		4	40	4	3.2
N78483	Hs.24809	ESTs		4	95	24	1.1
U90551	Hs.28777	H2A histone family; member L		4	350	88	3
AA010163	Hs.3383	upstream regulatory element binding protein 1		4	140	35	1.8
W60186	Hs.169487	ESTs		4	452	114	2
L04656		carbonic anhydrase VIII		3.9	39	8	3.6

FIGURE 10
(CONT.)

M27492	Hs.82112	interleukin 1 receptor; type I	3.9	39	2	3.5
X87613	Hs.169344	H.sapiens mRNA for skeletal muscle abundant protein	3.9	43	11	1
Y09443	Hs.22580	alkylglycerone phosphate synthase	3.9	49	13	2.5
AA227448	Hs.5003	Homo sapiens mRNA for KIAA0456 protein; partial cds	3.9	39	6	3.2
AA235303	Hs.8645	ESTs	3.9	79	20	6.5
AA398197	Hs.30029	ESTs	3.9	371	94	4.6
AA609210	Hs.19221	ESTs	3.9	98	25	8.6
N36001	Hs.17348	ESTs; Weakly similar to alternatively spliced product using	3.9	353	90	1.2
N67437	Hs.24375	ESTs	3.9	146	37	9.8
AA427528	Hs.114547	ESTs; Weakly similar to ZINC FINGER PROTEIN 84 [H.sa	3.9	39	8	2.2
AA521080	Hs.46765	ESTs	3.9	39	10	0.6
AA255933	Hs.109111	ESTs	3.9	161	42	2
AA400412	Hs.97794	ESTs	3.9	39	1	0.2
AA425374	Hs.193063	ESTs	3.9	39	1	0.2
AA600121	Hs.190253	ESTs	3.9	39	1	3.2
AA609471	Hs.112712	ESTs	3.9	39	5	3.7
AA370120	Hs.7870	ESTs; Weakly similar to Ylr350wp [S.cerevisiae]	3.9	47	12	4.4
H02682	Hs.99189	ESTs; Weakly similar to novel stromal cell protein [M.mus	3.9	220	57	2.5
M28879	Hs.1051	granzyme B (granzyme 2; cytotoxic T-lymphocyte-associa	3.9	43	11	1.8
D13435	Hs.166982	phosphatidylinositol glycan; class F	3.9	54	14	5.1
N21679	Hs.180059	ESTs	3.9	39	1	1.9
D31263	Hs.15929	ESTs	3.9	39	1	2.6
AA477739	Hs.246856	ESTs	3.9	39	1	3.4
R49035	Hs.26176	ESTs	3.9	116	30	0.5
U66615	Hs.172280	SWI/SNF related; matrix associated; actin dependent regu	3.9	39	1	2.5
U23070	Hs.78776	Human putative transmembrane protein (nma) mRNA; co BCH9	3.9	442	114	1.3
N22107	Hs.172241	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARBCN7	3.9	322	83	4.4
AA609651	Hs.112742	ESTs BCX7	3.9	60	16	4.8
K01160		Accession not listed in Genbank	3.9	390	100	11.1
AA057193	Hs.25252	ESTs	3.9	280	72	3.3
D28137	Hs.118110	bone marrow stromal cell antigen 2	3.8	350	93	1.9
J05249	Hs.79411	replication protein A2 (32kD)	3.8	115	30	7.1
S80562	Hs.194662	calponin 3; acidic	3.8	399	105	3.3
U28368	Hs.34853	inhibitor of DNA binding 4; dominant negative helix-loop-h	3.8	163	43	0.5
U57721	Hs.81771	kynureninase; l-kynurenine hydrolase	3.8	38	1	1.5
Z74615	Hs.172928	collagen; type I; alpha 1	3.8	1612	429	3.1
R86920	Hs.127585	ESTs	3.8	38	4	1.2
AA027317	Hs.221929	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING	3.8	40	11	3.8
AA084602	Hs.29669	ESTs	3.8	38	1	2.4
AA179826	Hs.32058	ESTs	3.8	38	2	3.2
AA233790	Hs.4104	ESTs	3.8	93	25	7.5
AA424006	Hs.22972	ESTs; Weakly similar to steroid 5-alpha-reductase 2 [H.sa	3.8	38	1	3.3
AA429951	Hs.21104	ESTs	3.8	83	22	7.5
AA436836	Hs.35580	ESTs	3.8	38	1	1.9
AA456646	Hs.28661	ESTs	3.8	263	69	3.9
AA489009	Hs.26994	ESTs	3.8	38	1	1.6
AA079468	Hs.94631	ESTs	3.8	38	1	3.2
AA179387	Hs.25264	ESTs	3.8	233	62	3.8
H42396	Hs.107872	ESTs	3.8	38	7	2.8
Z38909	Hs.22265	ESTs	3.8	73	19	1.8
AA478729	Hs.76450	ESTs	3.8	38	7	2.1
AA347422	Hs.238040	ESTs; Weakly similar to hypothetical protein [H.sapiens]	3.8	38	7	0.2
AA485458	Hs.181357	ESTs; Moderately similar to laminin-binding protein [H.sap	3.8	207	55	5.5
H05323	Hs.247486	ESTs	3.8	58	16	5.5
AA512902	Hs.7337	ESTs	3.8	38	1	3
N75007	Hs.199009	ESTs; Weakly similar to (defline not available 4589652) [H	3.8	38	1	0.9
AA232276	Hs.22806	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING	3.8	42	11	0.6
AA465527	Hs.23853	ESTs	3.8	38	1	3.3
AA418039	Hs.26155	ESTs	3.8	38	1	3
AA262821	Hs.28578	ESTs	3.8	79	21	6.9

FIGURE 10
(CONT.)

AA599653	Hs.30696	transcription factor-like 5 (basic helix-loop-helix)		3.8	51	14	1.7
AA448297	Hs.237825	calcium/calmodulin-dependent protein kinase (CaM kinas		3.8	38	1	3
AA174183	Hs.93872	ESTs		3.8	240	64	3.2
C00038	Hs.23579	ESTs	BCQ5	3.8	585	153	3.7
N91023	Hs.170057	ESTs	BCW4	3.8	425	111	4
AA007160	Hs.14846	ESTs	CQA2	3.8	82	22	3.1
AI167942	Hs.61635	Homo sapiens BAC clone RG041D11 from 7q21	PAA5	3.8	38	1	2.7
AA569531	Hs.162859	ESTs	PAA6	3.8	38	7	3.4
HG4297-HT4567		Transcriptional Coactivator Pc4		3.7	477	130	3.1
X53961	Hs.347	lactotransferrin		3.7	1421	388	1.9
AA434508		"zw31c1.r1 Soares ovary tumor NbHOT Homo sapiens cD		3.7	37	7	2.1
R64534	Hs.101469	ESTs		3.7	37	5	2.5
AA126855	Hs.13268	ESTs		3.7	157	43	3.6
AA128548	Hs.90847	ESTs; Weakly similar to Similarity with yeast transcription		3.7	37	1	3.2
H03627	Hs.245209	ESTs		3.7	37	4	2
H53572	Hs.32407	ESTs		3.7	37	1	2.1
N68869	Hs.15119	ESTs		3.7	119	33	6.7
R52949	Hs.25978	ESTs		3.7	37	1	3
W80763	Hs.3849	ESTs; Moderately similar to FK506-binding protein 65kD [		3.7	239	65	3.6
AA504116	Hs.82501	ESTs		3.7	37	1	1.8
N94475	Hs.227342	H.sapiens mRNA similar to Xenopus laevis mRNA for KDE		3.7	37	6	0.5
R46061	Hs.92482	ESTs		3.7	37	4	3
W84767	Hs.58698	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING		3.7	37	4	1.9
W86835	Hs.14158	copine III		3.7	590	159	3.8
AA280738	Hs.128679	ESTs		3.7	37	1	0.5
AA399441	Hs.104699	ESTs		3.7	37	10	1
AA495812	Hs.105364	ESTs		3.7	41	11	1.6
R28587	Hs.11000	Homo sapiens brain my047 protein mRNA; complete cds		3.7	39	11	3.2
M87339	Hs.35120	replication factor C (activator 1) 4 (37kD)		3.7	37	1	3.4
F09788	Hs.3622	procollagen-proline; 2-oxoglutarate 4-dioxygenase (prolin		3.7	37	9	2.8
X75535	Hs.168670	peroxisomal farnesylated protein		3.7	37	1	2.2
D15050	Hs.232068	"Human mRNA for transcription factor AREB6, complete c		3.7	91	25	2.6
W58612	Hs.173840	ESTs		3.7	41	11	0.6
AA121315	Hs.70823	KIAA1077 protein	BCU1	3.7	625	168	3.8
AA477445	Hs.105341	ESTs		3.7	162	44	12.4
AA477571	Hs.152601	UDP-glucose ceramide glucosyltransferase		3.7	224	61	21
D86978	Hs.84790	Human mRNA for KIAA0225 gene; partial cds		3.6	36	7	3.2
M55542	Hs.62661	guanylate binding protein 1; interferon-inducible; 67kD		3.6	36	1	2.6
M81057	Hs.180884	carboxypeptidase B1 (tissue)		3.6	824	227	1.4
U90304	Hs.25351	iroquois-class homeodomain protein		3.6	142	39	1.6
AA282138	Hs.11325	ESTs		3.6	36	1	0.1
AA398346	Hs.21898	ESTs		3.6	68	19	6
AA399623	Hs.23505	ESTs		3.6	36	7	3.1
AA400517	Hs.22983	ESTs; Moderately similar to UDP-GLUCOSE:GLYCOPRO		3.6	45	13	1.3
AA417287	Hs.171391	C-terminal binding protein 2		3.6	444	125	4.6
AA417761	Hs.5957	Homo sapiens clone 24416 mRNA sequence		3.6	365	103	6.9
AA461495	Hs.14512	ESTs		3.6	210	58	4.7
AA489665	Hs.25245	ESTs		3.6	36	1	1.2
D59368	Hs.159872	ESTs		3.6	36	6	0.5
H53829	Hs.36823	ESTs		3.6	36	10	2.5
T93630	Hs.17207	ESTs		3.6	36	4	2.6
AA456020	Hs.50848	ESTs; Weakly similar to (defline not available 4239895) [H		3.6	36	1	2
F01601	Hs.117485	ESTs		3.6	36	1	1.9
H99959	Hs.42768	ESTs; Weakly similar to (defline not available 4689264) [H		3.6	41	12	2.8
N66413	Hs.172466	ESTs; Weakly similar to (defline not available 3882271) [H		3.6	89	25	0.9
W73788	Hs.43213	ESTs		3.6	36	1	2.9
AA280794	Hs.241328	ESTs		3.6	36	8	0.2
AA426270	Hs.145696	ESTs		3.6	150	42	3.2
AA465196	Hs.107233	ESTs		3.6	36	1	3.4
W38240		Accession not listed in Genbank		3.6	38	11	2.6

FIGURE 10
(CONT.)

AA714635	Hs.181297	ESTs		3.6	36	6	2.9
AA305536		"EST176522 Colon carcinoma (Caco-2) cell line II Homo s		3.6	121	34	11.8
AA129640	Hs.128065	ESTs		3.6	36	10	1.9
D00763	Hs.243746	proteasome (prosome; macropain) subunit; alpha type; 4		3.6	130	36	3.5
D86959	Hs.105751	KIAA0204 gene product		3.6	36	5	1.5
X55330	Hs.207776	aspartylglucosaminidase		3.6	36	1	2.7
M95767	Hs.135578	chitobiase; di-N-acetyl-		3.6	36	1	1.2
AA248406	Hs.19347	ESTs		3.6	100	28	6.6
AA234767	Hs.246093	ESTs		3.6	141	39	12.6
AA479933	Hs.46967	ESTs		3.6	36	1	3.1
AA287107	Hs.172945	ESTs; Weakly similar to ZINC FINGER PROTEIN 135 [H.		3.6	146	41	1.1
U69611	Hs.64311	a disintegrin and metalloproteinase domain 17 (tumor nec		3.6	36	1	3.1
AA284143	Hs.194369	Homo sapiens chromosome 1 atrophin-1 related protein (		3.6	39	11	0.4
U30827	Hs.166975	Human splicing factor SRp40-1 (SRp40) mRNA; complete		3.6	36	1	0.4
X76040	Hs.250165	Lon protease-like protein		3.6	36	1	2.8
N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapiens]	BCW3	3.6	402	112	4.9
T95333	Hs.122730	ESTs; Weakly similar to Strabismus [D.melanogaster]	CVA9	3.6	224	63	4
H95039	Hs.32168	ESTs		3.6	282	79	1.7
AA609710	Hs.42582	ESTs; Weakly similar to similar to GTP-binding protein [C.		3.6	256	72	3.7
D42084	Hs.82007	Human mRNA for KIAA0094 gene; partial cds		3.5	96	28	1.3
D80004	Hs.75909	Human mRNA for KIAA0182 gene; partial cds		3.5	78	23	4.8
D87453	Hs.122669	Human mRNA for KIAA0264 gene; partial cds		3.5	35	9	3.1
HG371-HT1063		"Mucin 1, Epithelial, Alt. Splice 6"		3.5	37	11	2.8
U90651	Hs.151461	embryonic ectoderm development protein		3.5	35	1	2.7
AA232215	Hs.14600	ESTs		3.5	35	7	2.7
AA258873	Hs.25242	ESTs		3.5	73	21	1.6
AA417034	Hs.23019	ESTs; Weakly similar to ZINC FINGER PROTEIN 135 [H.		3.5	53	15	1.2
AA482035	Hs.28070	KIAA0753 gene product		3.5	58	17	1.6
AA504144	Hs.22315	ESTs		3.5	180	52	2.3
T74445	Hs.5957	"yc82f8.r1 Soares infant brain 1NIB Homo sapiens cDNA		3.5	35	1	2.6
AA016021	Hs.173091	Homo sapiens HCG-1 protein (HCG-1) mRNA; complete c		3.5	282	80	3.7
AA025315	Hs.61184	ESTs		3.5	35	1	1
AA129968	Hs.49376	ESTs; Weakly similar to PROTEIN PHOSPHATASE PP2A		3.5	35	1	3.2
H89315		"yw25e09.s1 Morton Fetal Cochlea Homo sapiens cDNA		3.5	35	8	1.9
N51374	Hs.96870	ESTs		3.5	35	9	3.2
R08850	Hs.9786	ESTs		3.5	35	1	2.1
R33468	Hs.24651	ESTs		3.5	105	30	9.6
R49482	Hs.5637	ESTs		3.5	507	145	3.3
R49483	Hs.22159	ESTs; Weakly similar to finger protein HZF10; Krueppel-re		3.5	40	12	2.5
R54822	Hs.26244	ESTs		3.5	41	12	3.7
T66847	Hs.194040	ESTs		3.5	35	1	1.4
W96222	Hs.34192	ESTs		3.5	35	6	3.2
AA459703	Hs.79070	ESTs; Moderately similar to coded for by C. elegans cDNA		3.5	35	8	3.3
N24954	Hs.42502	ESTs		3.5	72	21	1.3
N89881	Hs.44577	ESTs		3.5	35	1	2.9
AA377296	Hs.97104	ESTs		3.5	37	11	0.1
AA410383	Hs.100431	B-cell-homing chemokine (ligand for Burkitt's lymphoma re		3.5	35	1	2.6
AA412151	Hs.235402	ESTs		3.5	143	41	2.6
AA428213	Hs.98523	ESTs		3.5	35	3	2.3
AA454103	Hs.110031	ESTs		3.5	35	1	3
AI479264	Hs.13058	ESTs		3.5	35	4	3.3
AA936428	Hs.128638	ESTs		3.5	35	1	3.1
AI369384		arylsulfatase D		3.5	113	33	1.7
U58522	Hs.155485	"Human huntingtin interacting protein (HIP2) mRNA, comp		3.5	79	23	2.5
U25997	Hs.25590	stanniocalcin		3.5	402	114	2.1
AA090617	Hs.247614	ESTs		3.5	35	1	2.5
AA599801	Hs.239507	ESTs		3.5	73	21	6.3
AA496037	Hs.60293	ESTs		3.5	110	32	2.1
N30704	Hs.238797	ESTs		3.5	35	7	2.1
X72755	Hs.77367	monokine induced by gamma interferon	BCA6	3.5	796	228	3.2

FIGURE 10
(CONT.)

W72838	Hs.58213	ESTs	BCH1	3.5	2073	595	2.1
R45698	Hs.21893	ESTs	CZA1	3.5	124	35	6.5
X54941	Hs.77550	CDC28 protein kinase 1		3.5	332	94	3.1
Y00815	Hs.75216	protein tyrosine phosphatase; receptor type; F		3.5	564	162	1.7
D31888	Hs.78398	Homo sapiens clone 24709 mRNA sequence		3.4	77	23	5.9
D87470	Hs.75400	Human mRNA for KIAA0280 gene; partial cds		3.4	34	1	1.2
X85750	Hs.79889	H.sapiens mRNA for transcript associated with monocyte		3.4	34	8	2.3
AA004211	Hs.30977	ESTs; Weakly similar to putative p150 [H.sapiens]		3.4	154	46	3
AA292711	Hs.29131	ESTs		3.4	34	1	3.1
AA400093	Hs.32271	ESTs; Weakly similar to !!!! ALU SUBFAMILY SP WARNIN		3.4	34	8	2.9
AA401633	Hs.22380	ESTs		3.4	34	1	1.5
AA412505	Hs.10653	ESTs		3.4	49	15	4.4
AA417067	Hs.13055	ESTs		3.4	116	35	2.2
D51235	Hs.82689	tumor rejection antigen (gp96) 1		3.4	251	74	23.7
AA044181	Hs.62677	ESTs		3.4	34	1	2.3
AA129933	Hs.71168	Homo sapiens clone 24674 mRNA sequence		3.4	34	1	2.8
AA156460	Hs.44229	ESTs		3.4	34	1	2.6
AA167708	Hs.52184	ESTs		3.4	71	21	2.4
N48603	Hs.14947	ESTs		3.4	115	34	2.4
N95837	Hs.169111	ESTs		3.4	314	91	2.4
AA456968	Hs.82669	ESTs		3.4	34	8	1
N79496	Hs.50824	EST		3.4	740	217	2.8
T78324	Hs.90905	ESTs		3.4	34	3	2.4
W73057	Hs.58272	ESTs; Moderately similar to alternatively spliced product u		3.4	34	1	2.5
AA171739	Hs.101590	ESTs		3.4	34	1	1.7
AA251973	Hs.143853	ESTs		3.4	34	4	0.1
AA406293	Hs.193498	ESTs		3.4	34	1	0.8
AA418988	Hs.98314	ESTs		3.4	34	10	0.7
AA598899	Hs.112493	ESTs		3.4	34	1	2.6
AA621348	Hs.227933	ESTs; Highly similar to (defline not available 5281121) [H.		3.4	80	24	3.8
R41933	Hs.140237	ESTs; Weakly similar to neuronal thread protein AD7c-NT		3.4	210	63	3.3
T91518		"ye20f05.s1 Stratagene lung (#937210) Homo sapiens cD		3.4	985	286	2.8
R56892	Hs.75544	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase		3.4	234	68	10.7
AA219081	Hs.242396	ESTs; Moderately similar to !!!! ALU SUBFAMILY SB2 WA		3.4	107	32	9.9
W46810	Hs.20521	HMT1 (hnRNP methyltransferase; S. cerevisiae)-like 2		3.4	525	154	5.3
X86098	Hs.3238	adenovirus 5 E1A binding protein		3.4	115	34	9.1
H96226	Hs.42151	ESTs		3.4	58	17	4
N41849	Hs.119410	Homo sapiens cytokine receptor related protein 4 (CYTOR		3.4	34	2	3
AA386264	Hs.5337	ESTs		3.4	193	58	12.3
X78627	Hs.75066	translin		3.4	178	53	8.8
C02374	Hs.7822	ESTs		3.4	91	27	8.5
C06270	Hs.8078	Homo sapiens clone FBD3 Cri-du-chat critical region mRN		3.4	34	5	2.6
AA481414	Hs.8868	golgi SNAP receptor complex member 1		3.4	179	52	1.5
AA262727	Hs.12144	ESTs		3.4	88	26	1.4
M77698	Hs.97496	YY1 transcription factor		3.4	475	142	2.5
AA215333	Hs.97101	ESTs	CXA1	3.4	169	50	9.1
X70683	Hs.83484	SRY (sex determining region Y)-box 4		3.4	496	144	1.6
N81017	Hs.42679	ESTs		3.4	118	35	2.3
HG2874-HT3018		Ribosomal Protein L39 Homolog		3.3	116	36	2.2
HG4036-HT4306		Retinoblastoma 1		3.3	33	1	0.8
M84605	Hs.957	Human putative opioid receptor mRNA; complete cds		3.3	36	11	2.4
U43286	Hs.118725	Human selenophosphate synthetase 2 (SPS2) mRNA; co		3.3	111	34	7.5
X68733	Hs.234726	alpha-1-antichymotrypsin		3.3	1497	458	2.1
Z35402	Hs.194657	"H.sapiens gene encoding E-cadherin, exon 3 and joined		3.3	745	229	1.8
AA251297	Hs.23439	ESTs		3.3	206	63	2.2
AA350771	Hs.17850	ESTs		3.3	98	30	4.7
AA427816	Hs.11803	ESTs		3.3	95	29	4.4
AA434441	Hs.173859	frizzled (Drosophila) homolog 7		3.3	97	30	6.4
AA487561	Hs.5566	ESTs; Highly similar to RAS-RELATED PROTEIN RAB-1A		3.3	696	214	1.8
AA598820	Hs.3530	TLS-associated serine-arginine protein		3.3	228	69	2.8

FIGURE 10
(CONT.)

AA137078	Hs.173648	ESTs	3.3	33	5	1.7
AA171529	Hs.183887	ESTs	3.3	33	1	2.9
AA227119	Hs.171558	sex comb on midleg (Drosophila)-like 2	3.3	39	12	1.5
H61560	Hs.161011	EST	3.3	33	1	1.8
H98653	Hs.188006	Homo sapiens mRNA for KIAA0878 protein; complete cds	3.3	138	42	3.6
N69287	Hs.21943	ESTs	3.3	33	1	1.1
R44538	Hs.140889	ESTs	3.3	33	10	2.3
W37382	Hs.11090	ESTs	3.3	744	227	2.5
W42845	Hs.14611	dual specificity phosphatase 11 (RNA/RNP complex 1-inte	3.3	180	54	2.1
Z39742	Hs.247047	ESTs	3.3	33	1	2.4
AA150043	Hs.11498	ESTs	3.3	168	51	7.3
AA261819	Hs.88367	ESTs	3.3	33	1	3
AA481256	Hs.88201	ESTs; Weakly similar to (defline not available 3859560) [H	3.3	106	33	9.8
D51276	Hs.81915	leukemia-associated phosphoprotein p18 (stathmin)	3.3	931	279	5.6
H91164	Hs.237404	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WA	3.3	33	1	2.3
N67889	Hs.49397	ESTs	3.3	81	25	1.5
N98488	Hs.161545	EST	3.3	36	11	0.6
R39261	Hs.90790	ESTs	3.3	167	51	2.6
W43000	Hs.159225	ESTs	3.3	33	8	0.9
W52480	Hs.56148	ESTs; Moderately similar to (defline not available 5360125	3.3	33	10	0.5
AA227837	Hs.210566	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WAR	3.3	33	10	2.8
AA347419	Hs.96870	ESTs	3.3	33	3	0.2
AA446190	Hs.99051	ESTs	3.3	53	16	4
AA480103	Hs.111730	ESTs	3.3	207	63	3.5
N53976	Hs.179864	ESTs	3.3	33	1	1.7
W72949	Hs.77495	Human mRNA for KIAA0242 gene; partial cds	3.3	34	11	3.2
H22147	Hs.245474	ESTs; Moderately similar to !!!! ALU SUBFAMILY SP WAR	3.3	33	9	0.9
U31875	Hs.152677	short-chain alcohol dehydrogenase family member	3.3	105	32	3
W15528	Hs.106390	ESTs	3.3	288	87	7.9
X84373	Hs.155017	nuclear receptor interacting protein 1	3.3	354	108	4
X60486	Hs.46423	H4 histone family; member G	3.3	979	298	2.2
AA176475	Hs.4864	Homo sapiens mRNA for KIAA0892 protein; partial cds	3.3	33	4	2.9
AA253330	Hs.5344	ESTs	3.3	909	274	3.2
N26645	Hs.58220	Homo sapiens clone 24723 mRNA sequence	3.3	61	19	5.1
AA142857	Hs.234896	ESTs; Highly similar to geminin [H.sapiens]	3.3	106	33	2.6
AA216562	Hs.69855	neuroblastoma RAS viral (v-ras) oncogene homolog	3.3	33	1	2.9
M33882	Hs.76391	myxovirus (influenza) resistance 1; homolog of murine (in	3.3	380	114	4.9
W84712	Hs.7753	calumenin	3.3	889	267	5
S80437	Hs.83190	"fatty acid synthase (3' region) [human, breast and HepG2	3.3	710	217	2
N21407	Hs.247471	ESTs	3.3	33	1	2
C15324	Hs.93668	ESTs	3.3	1296	394	2.2
D30756	Hs.244822	membrane component; chromosome 17; surface marker 2	3.3	33	1	2.6
T32108	Hs.153315	ESTs CHA4	3.3	571	171	2
AA456687	Hs.26057	ESTs	3.3	775	233	2.4
D86969	Hs.82292	KIAA0215 gene product	3.2	32	2	2.9
X06272	Hs.75730	signal recognition particle receptor ('docking protein')	3.2	58	18	5
X15875	Hs.198166	activating transcription factor 2	3.2	32	4	2.6
Z35491	Hs.41714	BCL2-associated athanogene	3.2	41	13	2.8
Z80781	Hs.249216	H2B histone family; member J	3.2	32	5	2.8
AA314389	Hs.203994	ESTs; Weakly similar to (defline not available 4502227) [H	3.2	32	9	2.7
D55869	Hs.173138	ESTs	3.2	32	7	2.4
AA088228	Hs.18272	ESTs	3.2	522	165	1.9
AA112361	Hs.10592	ESTs	3.2	32	4	2.9
AA148859	Hs.179909	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARN	3.2	32	1	3
AA255874	Hs.23458	ESTs	3.2	466	146	8.4
AA256996	Hs.3862	ESTs	3.2	32	6	1.5
AA279991	Hs.124691	ESTs	3.2	32	1	1
AA369245	Hs.17448	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WAR	3.2	143	46	3.6
AA419609	Hs.170121	ESTs; Weakly similar to ETX1 (alternatively spliced) [H.sa	3.2	267	83	2.3
AA436628	Hs.158249	KIAA0406 gene product	3.2	37	12	2.6

FIGURE 10
(CONT.)

T63174	Hs.193700	ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WAR	3.2	110	35	9.6
AA004806	Hs.60090	ESTs	3.2	32	5	2.1
AA111879	Hs.69507	EST	3.2	32	5	1.7
AA180453	Hs.73643	ESTs	3.2	32	1	2.2
AA233342	Hs.90680	ESTs; Weakly similar to Unknown gene product [H.sapien	3.2	286	91	5.7
F10024	Hs.220640	ESTs	3.2	41	13	3.3
H09594	Hs.10299	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WA	3.2	136	43	3.6
R38436	Hs.21181	ESTs	3.2	37	12	3.5
T23860	Hs.7312	ESTs	3.2	99	31	3.1
W60002	Hs.4114	plastin 3 (T isoform)	3.2	238	75	2.1
AA258116	Hs.191533	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNI	3.2	49	16	4.2
AA435946	Hs.50831	ESTs	3.2	40	13	0.7
AA496000	Hs.4084	ESTs	3.2	173	55	3
N30205	Hs.93740	ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WAR	3.2	35	11	0.7
N66763	Hs.43080	ESTs	3.2	378	117	2.8
Z41050	Hs.108787	Homo sapiens Mcd4p homolog mRNA; complete cds	3.2	106	34	3.3
AA279654	Hs.194524	ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WAR	3.2	32	5	0.6
AA287389	Hs.98267	ESTs	3.2	32	8	3
AA416568	Hs.98203	ESTs	3.2	32	1	0.8
AA431751	Hs.106711	eukaryotic translation initiation factor 4E binding protein 3	3.2	88	28	1.2
AA449121	Hs.99210	ESTs	3.2	291	91	4
AA454149	Hs.99357	EST	3.2	32	10	3.1
AA460324	Hs.99527	ESTs	3.2	36	11	2.5
H90150	Hs.13366	Homo sapiens mRNA; cDNA DKFZp566F133 (from clone	3.2	32	1	1.5
W78134	Hs.122647	N-myristoyltransferase 2	3.2	37	12	3.6
AA488132	Hs.62741	ESTs	3.2	32	10	2.9
L12350	Hs.108623	thrombospondin 2	3.2	814	257	2.4
J04076	Hs.1395	early growth response 2 (Krox-20 (Drosophila) homolog)	3.2	32	1	0.2
D80074	Hs.169833	ESTs; Highly similar to (defline not available 4689144) [H.	3.2	87	27	1.7
H44386	Hs.22666	ESTs	3.2	210	66	3.8
U26174	Hs.3066	granzyme K (serine protease; granzyme 3; tryptase II)	3.2	82	26	6.6
N51260	Hs.196275	ESTs	3.2	207	64	5.5
X52947	Hs.74471	gap junction protein; alpha 1; 43kD (connexin 43)	3.2	351	111	5.2
Y00264	Hs.177486	amyloid beta (A4) precursor protein (protease nexin-II; Alz	3.2	226	71	2.8
L08044	Hs.169224	trefoil factor 3 (intestinal)	3.2	1872	592	3.3
X04011	Hs.88974	cytochrome b-245; beta polypeptide (chronic granulomato	3.2	143	45	13.9
X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	3.2	153	48	4.7
L14922	Hs.166563	replication factor C (activator 1) 1 (145kD)	3.2	32	1	2.4
M23263	Hs.99915	androgen receptor (dihydrotestosterone receptor; testicula	3.2	117	37	9.4
AA156897	Hs.72157	ESTs; Highly similar to (defline not available 4884194) [H.	BCU3 3.2	725	227	3.2
AA521354	Hs.24758	ESTs	BCW1 3.2	266	83	1.8
D21255	Hs.75929	cadherin 11 (OB-cadherin; osteoblast)	3.2	560	174	2.6
AA404352	Hs.178603	ESTs	3.2	372	115	2.1
D43772	Hs.86859	growth factor receptor-bound protein 7	3.1	306	98	1.5
L20320	Hs.184298	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cd	3.1	118	38	2
M55998		"Human alpha-1 collagen type I gene, 3' end"	3.1	2898	923	2.2
M93036	Hs.692	membrane component; chromosomal 4; surface marker (3	3.1	353	116	2.8
U27185	Hs.32943	retinoic acid receptor responder (tazarotene induced) 1	3.1	31	1	1.3
AA148516	Hs.35156	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARN	3.1	31	1	2.5
AA447223	Hs.25320	ESTs	3.1	72	23	5
AA448850	Hs.17138	ESTs	3.1	165	54	1.6
AA449741	Hs.4029	Glioma-amplified sequence-41	3.1	31	1	2.6
AA599472	Hs.247309	eukaryotic translation elongation factor 1 delta (guanine n	3.1	55	18	3.8
AA600310	Hs.18720	ESTs; Highly similar to (defline not available 4323587) [H.	3.1	75	24	2.2
AA609053	Hs.35198	ESTs	3.1	367	119	2.3
AA025782	Hs.61284	ESTs	3.1	31	9	2.2
AA135894	Hs.194691	retinoic acid induced 3	3.1	529	170	4.1
N29454	Hs.27552	ESTs; Weakly similar to putative p150 [H.sapiens]	3.1	31	1	2.7
N40981	Hs.9856	ESTs	3.1	31	1	1.3
T92735	Hs.17061	ESTs	3.1	453	148	7

FIGURE 10
(CONT.)

Z38239	Hs.26962	ESTs		3.1	31	5	1.5
AA417375	Hs.76917	ESTs; Weakly similar to KIAA0522 protein [H.sapiens]		3.1	58	19	2.5
AA620761	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (from clone		3.1	119	39	2
C20652	Hs.68501	ESTs		3.1	31	4	1.9
H95785	Hs.167652	ESTs; Highly similar to CENP-E protein [H.sapiens]		3.1	38	13	1.7
H98153	Hs.42500	ESTs		3.1	295	96	27.9
N49967	Hs.46624	ESTs		3.1	31	1	2.7
N66845	Hs.165411	ESTs; Weakly similar to !!!! ALU CLASS B WARNING EN		3.1	199	64	1
AA382275	Hs.97128	ESTs		3.1	31	1	0.4
AA436890	Hs.98918	ESTs		3.1	31	1	1
AA449453	Hs.192915	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING		3.1	31	6	0.8
AA608588	Hs.193634	ESTs		3.1	927	295	2.1
H88296	Hs.5123	ESTs; Weakly similar to (defline not available 4960208) [H		3.1	41	14	2.7
N50641	Hs.80285	ESTs		3.1	31	1	1.8
T90297	Hs.140571	ESTs		3.1	31	6	2.4
W42680	Hs.95941	ESTs		3.1	31	1	2.8
AA643322		"nr59c06.s1 NCI_CGAP_Lym3 Homo sapiens cDNA clon		3.1	31	1	2.5
AA625690	Hs.190272	ESTs		3.1	33	11	2.3
AI354332	Hs.72365	ESTs		3.1	31	8	2
AA093378	Hs.101810	ESTs; Weakly similar to !!!! ALU SUBFAMILY SC WARNIN		3.1	172	55	3.1
R48943	Hs.10315	solute carrier family 7 (cationic amino acid transporter; y+		3.1	31	1	2.2
W93562	Hs.105749	Homo sapiens mRNA for KIAA0553 protein; partial cds		3.1	34	11	2.7
F11087	Hs.239666	ESTs		3.1	31	2	2.5
T71333	Hs.13854	ESTs		3.1	31	3	3
M31627	Hs.149923	X-box binding protein 1		3.1	1336	434	1.4
AA121127	Hs.181307	ESTs		3.1	197	63	18.7
W01996	Hs.3945	ESTs; Highly similar to (defline not available 4929683) [H.		3.1	227	73	16.8
AA393804	Hs.67052	H beta 58 homolog		3.1	359	118	2.5
AA235289	Hs.247630	ESTs; Highly similar to rap2 gene product [H.sapiens]		3.1	234	76	8.6
D63477	Hs.84087	Human mRNA for KIAA0143 gene; partial cds		3.1	147	48	12.7
AC000115	Hs.9030	Human DNA sequence from PAC 196E23 on chromosom		3.1	31	1	2.3
U84011	Hs.904	amylo-1;6-glucosidase; 4-alpha-glucanotransferase (glyco		3.1	31	1	2.6
M74093	Hs.9700	cyclin E1		3.1	31	1	2.3
N75308	Hs.99433	ESTs		3.1	31	10	1.7
X54925	Hs.83169	matrix metalloproteinase 1 (interstitial collagenase)	AAC1	3.1	94	30	5.8
X12876	Hs.65114	keratin 18		3.1	815	266	1.7
M34309	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral oncogene hom		3	68	23	2.8
AA293300	Hs.9598	ESTs; Weakly similar to semaphorin C [M.musculus]	BCF1	3	30	10	0.9
AA609773	Hs.250175	Homo sapiens clone 23904 mRNA sequence	BCR2	3	816	275	3.9
AA505133	Hs.62273	ESTs	CAA2	3	380	127	5.5
HG2981-HT3127		"Epican, Alt. Splice 11"		3	594	201	2.3
AA195936	Hs.76362	general transcription factor IIA; 1 (37kD and 19kD subunit	BCF5	2.9	114	39	9.9
AA419622	Hs.104800	ESTs	BCN1	2.9	214	74	3.7
R53457	Hs.26040	ESTs	BCX1	2.8	751	270	1.3
AA234561	Hs.22862	ESTs	BCZ1	2.8	131	47	3.9
AA428062	Hs.98558	ESTs	BCU7	2.7	864	321	0.6
AA620795	Hs.8207	ESTs	BCQ8	2.5	392	155	4.3
AA449749	Hs.31386	ESTs; Highly similar to secreted apoptosis related protein	BCW8	2.1	1561	757	1.7
C13992	Hs.93668	ESTs	BCQ7	1.8	1047	596	1.6
H85169	Hs.172455	solute carrier family 5 (inositol transporters); member 3	BCW2	1	1	1	1

FIGURE 11

Accession	UniGene ID	UniGene Title		ratio tumor/ body	90%tile tumor	75%tile body	ratio tumor/ normal breast
AA126474	Hs.155223	stanniocalcin 2		72.2	722	1	1.9
AA434329	Hs.36563	ESTs	BCJ7	40.2	402	1	4
AA250737	Hs.72472	ESTs	BCY2	35.9	359	10	29.7
X82153	Hs.83942	cathepsin K (pycnodysostosis)		34.3	411	12	5.1
X03635	Hs.1657	estrogen receptor 1	BCQ3	32.2	322	1	4.7
H09290	Hs.76550	ESTs; Weakly similar to unknown [H.sapiens]		30.6	306	4	26.5
AA428090	Hs.26102	ESTs	BCN2	29	290	1	26.8
AA419547	Hs.11713	ESTs		26.3	356	14	1
AA256485	Hs.182471	ESTs	BCO2	25.4	508	20	3
N67239	Hs.10760	ESTs	BCX9	25.1	288	12	6.7
Z38595	Hs.125019	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING	BCY3	24.2	242	10	5.6
H25836	Hs.83429	tumor necrosis factor (ligand) superfamily; member 10		22.8	228	9	12.4
HG1763-HT1780		Prolactin-Induced Protein		22.7	760	34	1.4
AA411621	Hs.8895	ESTs		21.2	212	6	17.4
N46252	Hs.29724	ESTs	BCX6	20.9	209	1	19.5
U05237	Hs.99872	fetal Alzheimer antigen		20.6	206	4	19.1
U48807	Hs.2359	dual specificity phosphatase 4		20.2	202	5	1.3
AA070801	Hs.51615	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNI		18.7	187	1	17
U28831	Hs.44566	Human protein immuno-reactive with anti-PTH polyclonal antibodies		18.6	186	10	1.5
AA292066	Hs.240802	ESTs; Weakly similar to Br140 [H.sapiens]		17.5	175	2	12.8
N26722	Hs.42645	ESTs	BCY5	17.4	174	9	6.9
AA291725	Hs.105700	secreted frizzled-related protein 4	BCX2	17.4	409	24	7.8
AA065217	Hs.169674	ESTs		16.2	162	1	4.2
D13666	Hs.136348	osteoblast specific factor 2 (fasciclin I-like)	BCA4	15.7	1030	66	5
AA621169	Hs.8687	ESTs	BCX8	15.6	156	7	10.8
L07615		"Human neuropeptide Y receptor Y1 (NPYY1) mRNA, exo		15.3	153	1	14.1
AA007234	Hs.30098	ESTs		14.9	149	1	6.4
F01831	Hs.14838	ESTs	BCX4	14.6	219	15	7.6
N66818	Hs.42179	ESTs	BCY6	14.5	145	1	2.4
H05509	Hs.24639	ESTs		14.2	142	1	9.5
AA149007	Hs.243954	ESTs		13.7	137	1	8.9
D12485	Hs.11951	phosphodiesterase I/nucleotide pyrophosphatase 1 (homo	BCA2	13.2	244	19	9.9
AA490262	Hs.15485	ESTs; Moderately similar to APXL gene product [H.sapien	BCU8	13.2	331	25	12.4
W93640	Hs.4779	ESTs		13.1	131	1	5.1
AA458761	Hs.18387	ESTs		12.7	311	25	2.4
Z48633	Hs.6940	H.sapiens mRNA for retrotransposon		12.4	124	6	10.8
AA227219	Hs.110826	Homo sapiens CAGF9 mRNA; partial cds		12.3	123	1	11.3
T97307	Hs.161720	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARN		12.3	129	11	11.7
D31352	Hs.31433	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNI		11.7	117	1	10.1
AA251089	Hs.94576	ESTs; Weakly similar to phosducin; retinal [H.sapiens]		11.5	115	1	6.9
AA224180	Hs.187579	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING		11.5	115	1	10
F11019	Hs.12696	ESTs		11.4	114	1	10
X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acetyltransferase)		10.8	706	66	9.2
H93575	Hs.227146	ESTs		10.5	105	1	9.9
F13673	Hs.99769	ESTs	BCN4	10.4	880	85	5.3
AA411745	Hs.239681	ESTs; Weakly similar to KIAA0554 protein [H.sapiens]		10.3	103	1	9.3
M90516	Hs.1674	glutamine-fructose-6-phosphate transaminase 1		10	100	1	7.6
AA425309	Hs.33287	nuclear factor I/B	BCQ1	9.9	483	49	1.8
AA487468	Hs.100686	ESTs; Moderately similar to secreted cement gland protei	BCX3	9.9	351	36	13.9
M23379	Hs.758	RAS p21 protein activator (GTPase activating protein) 1		9.6	96	1	8.5
T25867	Hs.7549	ESTs	BCY9	9.6	124	13	9
R63542	Hs.110488	ESTs		9.5	95	1	8.5
M69225	Hs.620	bullous pemphigoid antigen 1 (230/240kD)		9.4	94	1	0.3
AI039722	Hs.171205	ESTs		9.4	94	3	5.3
U18321	Hs.159627	Death associated protein 3		9.3	93	5	8
AA283006	Hs.50758	chromosome-associated polypeptide C		9.3	93	1	8.4
U44378	Hs.75862	MAD (mothers against decapentaplegic; Drosophila) hom		9.3	93	1	7.8

FIGURE 11
(CONT.)

AA235112	Hs.106227	ESTs; Moderately similar to similar to murine RNA-binding		9.1	91	1	7.6
AA028028	Hs.61460	ESTs	BCX5	9	90	1	5.5
M77142	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protein		8.9	89	5	8
HG2981-HT3125		"Epican, Alt. Splice 1"		8.5	85	1	3.2
U33147	Hs.46452	mammaglobin 1		8.5	2058	243	1.4
AA280036	Hs.145374	ESTs; Weakly similar to W01A6.c [C.elegans]		8.5	127	15	1.6
AA609200	Hs.162686	ESTs	BCY4	8.5	85	1	4.3
D83004	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous to yeast U		8.5	85	1	7.2
AA257971	Hs.21214	ESTs		8.3	83	3	1.8
U59863	Hs.146847	TRAF family member-associated NFKB activator		8.2	82	1	6.8
T16387	Hs.65328	ESTs		8.2	82	1	6.4
H13108	Hs.107968	ESTs		8.2	82	1	7.4
D31161	Hs.68613	ESTs		8.1	81	1	4.6
M28213	Hs.78305	RAB2; member RAS oncogene family		7.8	78	1	5.6
AA031357	Hs.31803	ESTs		7.7	77	1	5.1
N66857	Hs.14808	ESTs; Weakly similar to !!!! ALU CLASS C WARNING EN		7.7	77	1	5
AA416997	Hs.59622	ESTs		7.6	144	19	13.9
R34531	Hs.243068	KIAA0480 gene product		7.6	76	1	5
W37145	Hs.30029	ESTs	PAA9	7.5	136	18	3.4
D60237	Hs.14368	SH3-binding domain glutamic acid-rich protein like		7.5	75	1	6.5
AA054228	Hs.23165	ESTs		7.4	74	1	6
M99701	Hs.95243	transcription elongation factor A (SII)-like 1		7.3	73	1	5.3
Z46629	Hs.2316	SRY (sex-determining region Y)-box 9 (campomelic dyspl		7.3	73	1	5.2
AA478446	Hs.69559	ESTs; Weakly similar to Bat2 [H.sapiens]		7.2	72	1	5.7
U83908	Hs.247134	Homo sapiens nuclear antigen H731-like protein mRNA; c		7.2	72	1	5.8
AA199828	Hs.188662	ESTs	BCY8	7.1	71	1	6.5
D61676	Hs.21851	Homo sapiens mRNA; cDNA DKFZp586J2118 (from clone	BCB9	7.1	392	56	3.6
AA211941	Hs.109643	polyadenylate binding protein-interacting protein 1		7.1	71	1	6.2
H18027	Hs.184697	receptor for virally-encoded semaphorin	BCY7	7.1	150	21	14.5
AA032147	Hs.23296	ESTs		7	70	1	6.5
AA292701	Hs.5364	ESTs		6.9	69	1	4.4
J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)		6.8	68	1	5.6
Z38763	Hs.15740	ESTs		6.7	67	1	6.3
AI287461	Hs.164950	ESTs		6.7	67	1	6
AA195260	Hs.204151	ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WAR		6.7	67	1	5.7
N29888	Hs.169539	ESTs		6.5	65	4	5.3
AA490862	Hs.55901	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WA		6.5	65	1	5.6
U37519	Hs.87539	aldehyde dehydrogenase 8		6.4	428	67	2.3
W23625	Hs.8739	ESTs		6.4	64	1	5.1
AA609723	Hs.30652	ESTs	PAA3	6.3	63	1	5.4
H10933	Hs.10067	ESTs	BCA1	6.3	693	110	7.2
N67711	Hs.151046	Homo sapiens clone 23859 mRNA sequence		6.3	63	1	5.8
AA430124	Hs.234607	ESTs		6.2	62	1	5.4
U35835	Hs.155637	protein kinase; DNA-activated; catalytic polypeptide		6.1	61	1	5.7
AA262491	Hs.186572	ESTs		5.8	58	1	5
D60302	Hs.108977	ESTs	BCY1	5.8	321	55	17
R51309	Hs.70823	KIAA1077 protein	BCN5	5.7	567	100	6.7
AA092376	Hs.90606	15 kDa selenoprotein		5.7	57	1	5
U90914	Hs.5057	carboxypeptidase D		5.6	56	1	5.3
AA130273	Hs.7584	ESTs; Weakly similar to (defline not available 4240269) [H	BCF3	5.5	55	1	5.2
AA491465	Hs.28792	ESTs	BCU9	4.7	381	81	6.4
AA047036	Hs.62817	ESTs	BCR9	4.6	427	93	10.4
U41060	Hs.79136	Human breast cancer; estrogen regulated LIV-1 protein (L	BCR4	4.5	1472	330	2.1
AA169379	Hs.72865	ESTs	BCU4	4.1	334	82	3.4
N22107	Hs.172241	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WAR	BCN7	3.9	322	83	4.4
AA609651	Hs.112742	ESTs	BCX7	3.9	60	16	4.8
N91023	Hs.170057	ESTs	BCW4	3.8	425	111	4
C00038	Hs.23579	ESTs	BCQ5	3.8	585	153	3.7
N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapiens]	BCW3	3.6	402	112	4.9
W72838	Hs.58213	ESTs	BCH1	3.5	2073	595	2.1

AA609773	Hs.250175	Homo sapiens clone 23904 mRNA sequence	BCR2	3	816	275	3.9
AA419622	Hs.104800	ESTs	BCN1	2.9	214	74	3.7
AA234561	Hs.22862	ESTs	BCZ1	2.8	131	47	3.9
AA620795	Hs.8207	ESTs	BCQ8	2.5	392	155	4.3
C13992	Hs.93668	ESTs	BCQ7	1.8	1047	596	1.6
H85169	Hs.172455	solute carrier family 5 (inositol transporters); member 3	BCW2	1	1	1	1

FIGURE 11
(CONT.)

FIGURE 12

Accession	UniGene ID	UniGene Title
W72838	Hs.58213	ESTs
D12485	Hs.11951	phosphodiesterase I (PC-1)
AA434329	Hs.36563	ESTs
AA419622	Hs.104800	ESTs
R51309	Hs.70823	KIAA1077 protein
AA256485	Hs.182471	ESTs
C00038	Hs.23579	ESTs
AA609773	Hs.250175	Homo sapiens clone 23904 mRNA sequence
AA291725	Hs.105700	secreted frizzled-related protein 4
Z38595	Hs.125019	ESTs

	ratio tumor/ body	90%tile tumor	75%tile body	ratio tumor/ normal breast
BCH1	3.5	2073	595	2.1
BCA2	13.2	244	19	9.9
BCJ7	40.2	402	1	4
BCN1	2.9	214	74	3.7
BCN5	5.7	567	100	6.7
BCO2	25.4	508	20	3
BCQ5	3.8	585	153	3.7
BCR2	3	816	275	3.9
BCX2	17.4	409	24	7.8
BCY3	24.2	242	10	5.6

GGGACAGGGCTGAGGATGAGGAGAACCCTGGGGACCCAGAAGACCGTGCCTTGCCCGGAAGTCCTGCCTGTAGGCCTGAA
GGACTTGCCCTAACAGAGCCTCAACAACTACCTGGTGATTCCTACTTCAGCCCCTTGGTGTGAGCAGCTTCTCAACATGA
ACTACAGCCTCCACTTGGCCTTCGTGTGTCTGAGTCTCTTCACTGAGAGGATGTGCATCCAGGGGAGTCAGTTCAACGTC
GAGGTCGGCAGAAGTGACAAGCTTTCCCTGCCTGGCTTTGAGAACCTCACAGCAGGATATAACAAATTTCTCAGGCCCAA
TTTTGGTGGAGAACCCGTACAGATAGCGCTGACTCTGGACATTGCAAGTATCTCTAGCATTTCAGAGAGTAACATGGACT
ACACAGCCACCATATACCTCCGACAGCGCTGGATGGACCAGCGGCTGGTGTTTGAAGGCAACAAGAGCTTCACTCTGGAT
GCCCGCCTCGTGGAGTTCCTCTGGGTGCCAGATACTTACATTGTGGAGTCCAAGAAGTCCTTCCTCCATGAAGTCACTGT
GGGAAACAGGCTCATCCGCCTCTTCTCCAATGGCACGGTCCTGTATGCCCTCAGAATCACGACAACTGTTGCATGTAACA
TGGATCTGTCTAAATACCCCATGGACACACAGACATGCAAGTTGCAGCTGGAAAGCTGGGGCTATGATGGAAATGATGTG
GAGTTCACCTGGCTGAGAGGGAACGACTCTGTGCGTGGACTGGAACACCTGCGGCTTGCTCAGTACACCATAGAGCGGTA
TTTCACCTTAGTCACCAGATCGCAGCAGGAGACAGGAAATTACACTAGATTGGTCTTACAGTTTGAGCTTCGGAGGAATG
TTCTGTATTTCATTTTGGAAACCTACGTTCCTTCCACTTTCCTGGTGGTGTTGTCCTGGGTTTCATTTTGGATCTCTCTC
GATTCAGTCCCTGCAAGAACCTGCATTGGAGTGACGACCGTGTTATCAATGACCACACTGATGATCGGGTCCCGCACTTC
TCTTCCCAACACCAACTGCTTCATCAAGGCCATCGATGTGTACCTGGGGATCTGCTTTAGCTTTGTGTTTGGGGCCTTGC
TAGAATATGCAGTTGCTCACTACAGTTCCTTACAGCAGATGGCAGCCAAAGATAGGGGGACAACAAAGGAAGTAGAAGAA
GTCAGTATTACTAATATCATCAACAGCTCCATCTCCAGCTTTAAACGGAAGATCAGCTTTGCCAGCATTGAAATTTCCAG
CGACAACGTTGACTACAGTGACTTGACAATGAAAACCAGCGACAAGTTCAAGTTTGTCTTCCGAGAAAAGATGGGCAGGA
TTGTTGATTATTTCACAATTCAAAACCCCAGTAATGTTGATCACTATTCCAAACTACTGTTTCCTTTGATTTTTATGCTA
GCCAATGTATTTTACTGGGCATACTACATGTATTTTTGAGTCAATGTTAAATTTCTTGCATGCCATAGGTCTTCAACAGG
ACAAGATAATGATGTAAATGGTATTTTAGGCCAAGTGTGCACCCACATCCAATGGTGCTACAAGTGACTGAAATAATATT
TGAGTCTTTCTGCTCAAAGAATGAAGCTCCAACCATTGTTCTAAGCTGTGTAGAAGTCCTAGCATTATAGGATCTTGTAA
TAGAAACATCAGTCCATTCCTCTTTCATCTTAATCAAGGACATTCCCATGGAGCCCAAGATTACAAATGTACTCAGGGCT
GTTTATTCGGTGGCTCCCTGGTTTGCATTTACCTCATATAAAGAATGGGAAGGAGACCATTGGGTAACCCTCAAGTGTCA
GAAGTTGTTTCTAAAGTAACTATACATGTTTTTTACTAAATCTCTGCAGTGCTTATAAAATACATTGTTGCCTATTTAGG
GAGTAACATTTTCTAGTTTTTGTTTCTGGTTAAAATGAAATATGGGCTTATGTCAATTCATTGGAAGTCAATGCACTAAC
TCAATACCAAGATGAGTTTTTAAATAATGAATATTATTTAATACCACAACAGAATTATCCCCAATTTCCAATAAGTCCTA
TCATTGAAAATTCAAATATAAGTGAAGAAAAAATTAGTAGATCAACAATCTAAACAAATCCCTCGGTTCTAAGATACAAT
GGATTCCCCATACTGGAAGGACTCTGAGGCTTTATTCCCCCACTATGCATATCTTATCATTTTATTATTATACACACATC
CATCCTAAACTATACTAAAGCCCTTTTCCCATGCATGGATGGAAATGGAAGATTTTTTTGTAACTTGTTCTAGAAGTCTT
AATATGGGCTGTTGCCATGAAGGCTTGCAGAATTGAGTCCATTTTCTAGCTGCCTTTATTCACATAGTGATGGGGTACTA
AAAGTACTGGGTTGACTCAGAGAGTCGCTGTCATTCTGTCATTGCTGCTACTCTAACACTGAGCAACACTCTCCCAGTGG
CAGATCCCCTGTATCATTCCAAGAGGAGCATTCATCCCTTTGCTCTAATGATCAGGAATGATGCTTATTAGAAAACAAAC
TGCTTGACCCAGGAACAAGTGGCTTAGCTTAAGTAAACTTGGCTTTGCTCAGATCCCTGATCCTTCCAGCTGGTCTGCTC
TGAGTGGCTTATCCCGCATGAGCAGGAGCGTGCTGGCCCTGAGTACTGAACTTTCTGAGTAACAATGAGACACGTTACAG
AACCTATGTTCAGGTTGCGGGTGAGCTGCCCTCTCCAAATCCAGCCAGAGATGCACATTCCTCGGCCAGTCTCAGCCAAC
AGTACCAAAAGTGATTTTTGAGTGTGCCAGGGTAAAGGCTTCCAGTTCAGCCTCAGTTATTTTAGACAATCTCGCCATCT
TTAATTTCTTAGCTTCCTGTTCTAATAAATGCACGGCTTTACCTTTCCTGTCAGAAATAAACCAAGGCTCTAAAAGATGA
TTTCCCTTCTGTAACTCCCTAGAGCCACAGGTTCTCATTCCTTTTCCCATTATACTTCTCACAATTCAGTTTCTATGAGT
TTGATCACCTGATTTTTTTAACAAAATATTTCTAACGGGAATGGGTGGGAGTGCTGGTGAAAAGAGATGAAATGTGGTTG
TATGAGCCAATCATATTTGTGATTTTTTAAAAAAAGTTTAAAAGGAAATATCTGTTCTGAAACCCCACTTAAGCATTGTT
TTTATATAAAAACAATGATAAAGATGTGAACTGTGAAATAAATATACCATATTAGCTACCCACC

FIGURE 13

FIGURE 14

ATGAACTACAGCCTCCACTTGGCCTTCGTGTGTCTGAGTCTCTTCACTGAGAGGATGTGCATCCAGGGGAGTCAGTTCAA
CGTCGAGGTCGGCAGAAGTGACAAGCTTTCCCTGCCTGGCTTTGAGAACCTCACAGCAGGATATAACAAATTTCTCAGGC
CCAATTTTGGTGGAGAACCCGTACAGATAGCGCTGACTCTGGACATTGCAAGTATCTCTAGCATTTCAGAGAGTAACATG
GACTACACAGCCACCATATACCTCCGACAGCGCTGGATGGACCAGCGGCTGGTGTTTGAAGGCAACAAGAGCTTCACTCT
GGATGCCCGCCTCGTGGAGTTCCTCTGGGTGCCAGATACTTACATTGTGGAGTCCAAGAAGTCCTTCCTCCATGAAGTCA
CTGTGGGAAACAGGCTCATCCGCCTCTTCTCCAATGGCACGGTCCTGTATGCCCTCAGAATCACGACAACTGTTGCATGT
AACATGGATCTGTCTAAATACCCCATGGACACACAGACATGCAAGTTGCAGCTGGAAAGCTGGGGCTATGATGGAAATGA
TGTGGAGTTCACCTGGCTGAGAGGGAACGACTCTGTGCGTGGACTGGAACACCTGCGGCTTGCTCAGTACACCATAGAGC
GGTATTTCACCTTAGTCACCAGATCGCAGCAGGAGACAGGAAATTACACTAGATTGGTCTTACAGTTTGAGCTTCGGAGG
AATGTTCTGTATTTCATTTTGGAAACCTACGTTCCTTCCACTTTCCTGGTGGTGTTGTCCTGGGTTTCATTTTGGATCTC
TCTCGATTCAGTCCCTGCAAGAACCTGCATTGGAGTGACGACCGTGTTATCAATGACCACACTGATGATCGGGTCCCGCA
CTTCTCTTCCCAACACCAACTGCTTCATCAAGGCCATCGATGTGTACCTGGGGATCTGCTTTAGCTTTGTGTTTGGGGCC
TTGCTAGAATATGCAGTTGCTCACTACAGTTCCTTACAGCAGATGGCAGCCAAAGATAGGGGGACAACAAAGGAAGTAGA
AGAAGTCAGTATTACTAATATCATCAACAGCTCCATCTCCAGCTTTAAACGGAAGATCAGCTTTGCCAGCATTGAAATTT
CCAGCGACAACGTTGACTACAGTGACTTGACAATGAAAACCAGCGACAAGTTCAAGTTTGTCTTCCGAGAAAAGATGGGC
AGGATTGTTGATTATTTCACAATTCAAAACCCCAGTAATGTTGATCACTATTCCAAACTACTGTTTCCTTTGATTTTTAT
GCTAGCCAATGTATTTTACTGGGCATACTACATGTATTTTTGA

FIGURE 15

MNYSLHLAFVCLSLFTERMCIQGSQFNVEVGRSDKLSLPGFENLTAGYNKFLRPNFGGEPVQIALTLDIASISSISESNM
DYTATIYLRQRWMDQRLVFEGNKSFTLDARLVEFLWVPDTYIVESKKSFLHEVTVGNRLIRLFSNGTVLYALRITTTVAC
NMDLSKYPMDTQTCKLQLESWGYDGNDVEFTWLRGNDSVRGLEHLRLAQYTIERYFTLVTRSQQETGNYTRLVLQFELRR
NVLYFILETYVPSTFLVVLSWVSFWISLDSVPARTCIGVTTVLSMTTLMIGSRTSLPNTNCFIKAID[redacted]
[redacted]HYSSLQQMAAKDRGTTKEVEEVSITNIINSSISSFKRKISFASIEISSDNVDYSDLTMKTSDKFKFVFREKMG
RIVDYFTIQNPSNVDHYSKLLFPLIFMLANVFYWAYYMYF.

FIGURE 16

BCR3p1

Ac-Ala-Cys-Asn-Met-Asp-Leu-Ser-Lys-Tyr-Pro-
Met-Asp-Thr-Gln-Thr-NH_2

Ac-Cys-Lys-Leu-Gln-Leu-Glu-Ser-Trp-Gly-Tyr
-Asp-Gly-Asn-Asp-Val-NH_2

BCR3p2

FIGURE 17

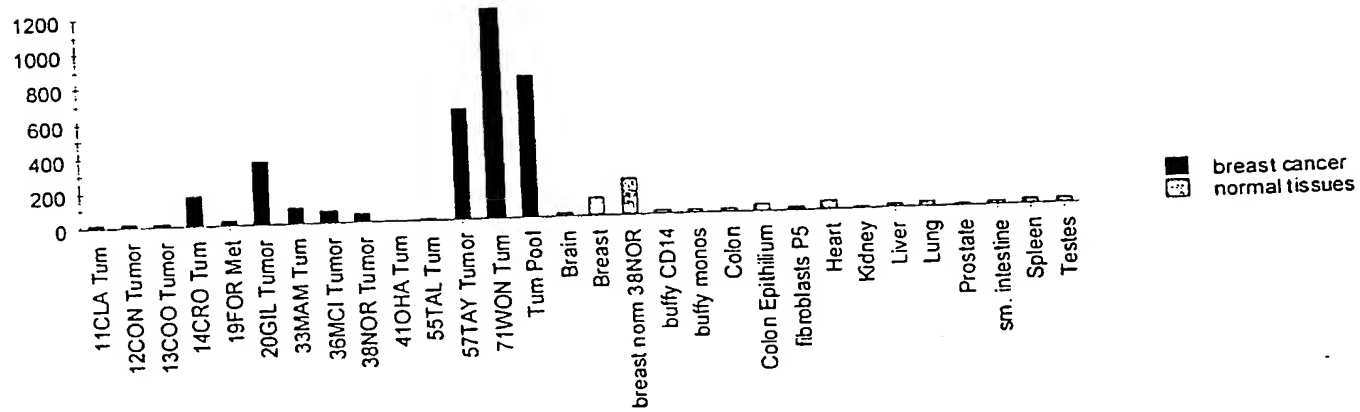


FIGURE 18

GTGAAGAGAGGCGCGGCGTGACTGAGCTACGGTTCTGGCTGCGTCCTAGAGGCATCCGGGGCAGTAAAACCGCTGCGATC
GCGGAGGCGGCGGCCAGGCCGAGAGCAGGCCGGGCAGGGGTGTCGGACGCAGGGCGCTGGGCCGGGTTTCGGCTTCGGCC
ACAGCTTTTTTTCTCAAGGTGCAATGAAAGCCTTCCACACTTTCTGTGTTGTCCTTCTGGTGTTTGGGAGTGTCTCTGAA
GCCAAGTTTGATGATTTTGAGGATGAGGAGGACATAGTAGAGTATGATGATAATGACTTCGCTGAATTTGAGGATGTCAT
GGAAGACTCTGTTACTGAATCTCCTCAACGGGTCATAATCACTGAAGATGATGAAGATGAGACCACTGTGGAGTTGGAAG
GGCAGGATGAAAACCAAGAAGGAGATTTTGAAGATGCAGATACCCAGGAGGGAGATACTGAGAGTGAACCATATGATGAT
GAAGAATTTGAAGGTTATGAAGACAAACCAGATACTTCTTCTAGCAAAAATAAAGACCCAATAACGATTGTTGATGTTCC
TGCACACCTCCAGAACAGCTGGGAGAGTTATTATCTAGAAATTTTGATGGTGACTGGTCTGCTTGCTTATATCATGAATT
ACATCATTGGGAAGAATAAAAACAGTCGCCTTGCACAGGCCTGGTTTAACACTCATAGGGAGCTTTTGGAGAGCAACTTT
ACTTTAGTGGGGGATGATGGAACTAACAAAGAAGCCACAAGCACAGGAAAGTTGAACCAGGAGAATGAGCACATCTATAA
CCTGTGGTGTTCTGGTCGAGTGTGCTGTGAGGGCATGCTTATCCAGCTGAGGTTCCTCAAGAGACAAGACTTACTGAATG
TCCTGGCCCGGATGATGAGGCCAGTGAGTGATCAAGTGCAAATAAAAGTAACCATGAATGATGAAGACATGGATACCTAC
GTATTTGCTGTTGGCACACGGAAAGCCTTGGTGCGACTACAGAAAGAGATGCAGGATTTGAGTGAGTTTTGTAGTGATAA
ACCTAAGTCTGGAGCAAAGTATGGACTGCCGGACTCTTTGGCCATCCTGTCAGAGATGGGAGAAGTCACAGACGGAATGA
TGGATACAAAGATGGTTCACTTCTTACACACCTATGCTGACAAGATTGAATCTGTTCATTTTTCAGACCAGTTCTCTGGT
CCAAAAATTATGCAAGAGGAAGGTCAGCCTTTAAAGCTACCTGACACTAAGAGGACACTGTTGTTTACATTTAATGTGCC
TGGCTCAGGTAACACTTACCCAAAGGATATGGAGGCACTGCTACCCCTGATGAACATGGTGATTTATTCTATTGATAAAG
CCAAAAAGTTCCGACTCAACAGAGAAGGCAAACAAAAAGCAGATAAGAACCGTGCCCGAGTAGAAGAGAACTTCTTGAAA
CTGACACATGTGCAAAGACAGGAAGCAGCACAGTCTCGGCGGGAGGAGAAAAAAAGAGCAGAGAAGGAGCGAATCATGAA
TGAGGAAGATCCTGAGAAACAGCGCAGGCTGGAGGAGGCTGCATTGAGGCGTGACGAAAAAGAAGTTGGAAAAGAAGCAA
ATGAAAATGAAACAAATCAAAGTGAAAGCCATGTAAAGCCATCCCAGAGATTTGAGTTCTGATGCCACCTGTAAGCTCTG
AATTCACAGGAAACATGAAAAACGCCAGTCCATTTCTCAACCTTAAATTTCAGACAGTCTTGGGCAACTGAGAAATCCTT
ATTTCATCATCTACTCTGTTTGGGGTTTGGGGTTTTACAGAGATTGAAGATACCTGGAAAGGGCTCTGTTTCAAGAATTT
TTTTTTCCAGATAATCAAATTATTTTGATTATTTTATAAAAGGAATGATCTATGAAATCTGTGTAGGTTTTAAATATTTT
AAAAATTATAATACAAATCATCAGTGCTTTTAGTACTTCAGTGTTTAAAGAAATACCATGAAATTTATAGGTAGATAACC
AGATTGTTGCTTTTTGTTTAAACCAAGCAGTTGAAATGGCTATAAAGACTGACTCTAAACCAAGATTCTGCAAATAATGA
TTGGAATTGCACAATAAACATTGCTTGATGTTTTCTTGTATGTCTACATTAAACTTGAGAAAAAGTAAAAATTAGAACAC
TGTATGTAGTAATGAAATTTCAGGGACCCAGAACATAATGTAGTATATGTTTTTAGGTGGGAGATGCTGATAACAAAATT
AATAGGAAGTCTGTAGGCATTAGGATACTGACATGTACATGGAAAATTCTAGGGACAGGAGCATCATTTTTTCCTTACCT
GATACCACGAACCAGTGACAACGTGAATGCTGTATTTTAAGTGGTTGTATGTTTATTTTCTTGAGTAACAAATGCATGAA
AAATTAATGCTTCACCTAGGTAAGATCATTGGTCTGTGTGAAATCACAAATGTTTTTTCCTTCTTGGTTGCTGCAGCCTG
GGTGGATGTTCATGGAGAAGCTCTGTTCTCTATATTATGGCTGTGTGCCGTTGCTTCTCCCTCTGCTTTTATCTTTTCCA
CAGTTGAGGCTGGGTATGTTCTTTCAAAGAAATGGCCATGAATATGTGTAAGTATACTTTTGAAAATGAGCTTTCCTAAA
CTATTGAGAGTTCTTTCCACCTCTTGCGGAACCAACTCTTGGAGGAGAGGCCCATGTATCTGCACGAGCACTTAGCTTGT
TCAGATCTCTGCATTTTATAAATGCTTCTTACCAAGAAAGCATTTTTAGGTCATTGCTTGTACCAGGTAATTTTTGCCGG
GGATGGGTAAGGGTTGGGTTTTCTGGTGGGAGTGGGGTGGTGGGTATTTTTTGTTGATGCTTTAGTGCAGGCCTGTTCTG
AGGCAATAACAAGTTGCTGTGAAAACAGCATGTGCTGCTGCCTTTGTAACTGCATGGAAACTTTTCACATGGGTTTTTCT
CCAAGTTAATACAGAAATATGTAAACTGAGAGATGCAAATGTAATATTTTTAACAGTTCATGAAGTTGTTATTAAAATAA
CTAACATAAAACTTAATTACTTTAATATTATATAATTATAGTAGTGGCCTTGTTTTACAAACCTTTAAATTACATTTTAG
AAATCAAAGTTGATAGTCTTAGTTATCTTTTGAGTAAGAAAAGCTTTCCTAAAGTCCCATACATTTGGACCATGGCAGCT
AATTTTGTAACTTAAGCATTCATATGAACTACCTATGGACATCTATTAAAGTGATTGACAAAATCTCAAAAAAAAAAAAA
AAAAAAAAAA

FIGURE 19

ATGAAAGCCTTCCACACTTTCTGTGTTGTCCTTCTGGTGTTTGGGAGTGTCTCTGAAGCCAAGTTTGATGATTTTGAGGA
TGAGGAGGACATAGTAGAGTATGATGATAATGACTTCGCTGAATTTGAGGATGTCATGGAAGACTCTGTTACTGAATCTC
CTCAACGGGTCATAATCACTGAAGATGATGAAGATGAGACCACTGTGGAGTTGGAAGGGCAGGATGAAAACCAAGAAGGA
GATTTTGAAGATGCAGATACCCAGGAGGGAGATACTGAGAGTGAACCATATGATGATGAAGAATTTGAAGGTTATGAAGA
CAAACCAGATACTTCTTCTAGCAAAAATAAAGACCCAATAACGATTGTTGATGTTCCTGCACACCTCCAGAACAGCTGGG
AGAGTTATTATCTAGAAATTTTGATGGTGACTGGTCTGCTTGCTTATATCATGAATTACATCATTGGGAAGAATAAAAAC
AGTCGCCTTGCACAGGCCTGGTTTAACACTCATAGGGAGCTTTTGGAGAGCAACTTTACTTTAGTGGGGGATGATGGAAC
TAACAAAGAAGCCACAAGCACAGGAAAGTTGAACCAGGAGAATGAGCACATCTATAACCTGTGGTGTTCTGGTCGAGTGT
GCTGTGAGGGCATGCTTATCCAGCTGAGGTTCCTCAAGAGACAAGACTTACTGAATGTCCTGGCCCGGATGATGAGGCCA
GTGAGTGATCAAGTGCAAATAAAAGTAACCATGAATGATGAAGACATGGATACCTACGTATTTGCTGTTGGCACACGGAA
AGCCTTGGTGCGACTACAGAAAGAGATGCAGGATTTGAGTGAGTTTTGTAGTGATAAACCTAAGTCTGGAGCAAAGTATG
GACTGCCGGACTCTTTGGCCATCCTGTCAGAGATGGGAGAAGTCACAGACGGAATGATGGATACAAAGATGGTTCACTTC
TTACACACCTATGCTGACAAGATTGAATCTGTTCATTTTTCAGACCAGTTCTCTGGTCCAAAAATTATGCAAGAGGAAGG
TCAGCCTTTAAAGCTACCTGACACTAAGAGGACACTGTTGTTTACATTTAATGTGCCTGGCTCAGGTAACACTTACCCAA
AGGATATGGAGGCACTGCTACCCCTGATGAACATGGTGATTTATTCTATTGATAAAGCCAAAAAGTTCCGACTCAACAGA
GAAGGCAAACAAAAAGCAGATAAGAACCGTGCCCGAGTAGAAGAGAACTTCTTGAAACTGACACATGTGCAAAGACAGGA
AGCAGCACAGTCTCGGCGGGAGGAGAAAAAAAGAGCAGAGAAGGAGCGAATCATGAATGAGGAAGATCCTGAGAAACAGC
GCAGGCTGGAGGAGGCTGCATTGAGGCGTGACGAAAAAGAAGTTGGAAAAGAAGCAAATGAAAATGAAACAAATCAAAGT
GAAAGCCATGTAAAGCCATCCCAGAGATTTGAGTTCTGA

FIGURE 20

MKAFHTFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDSVTESPQRVIITEDDEDETTVELEGQDENQEG
DFEDADTQEGDTESEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWESYYLEYLMVTGLLAYIMNYIIGKNKN
SRLAQAWFNTHRELLESNFTLVGDEGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFLKRQDLLNVLARMMRP
VSDQVQIKVTMNDEDMDTYVFAVGTRKALVRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMMDTKMVHF
LHTYADKIESVHFSDQFSGPKIMQEEGQPLKLPDTKRTLLFTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNR
EGKQKADKNRARVEENFLKLTHVQRQEAAQSRREEKKRAEKERIMNEEDPEKQRRLEEAALRRDEKEVGKEANENETNQS
ESHVKPSQRFEF.

FIGURE 2 1

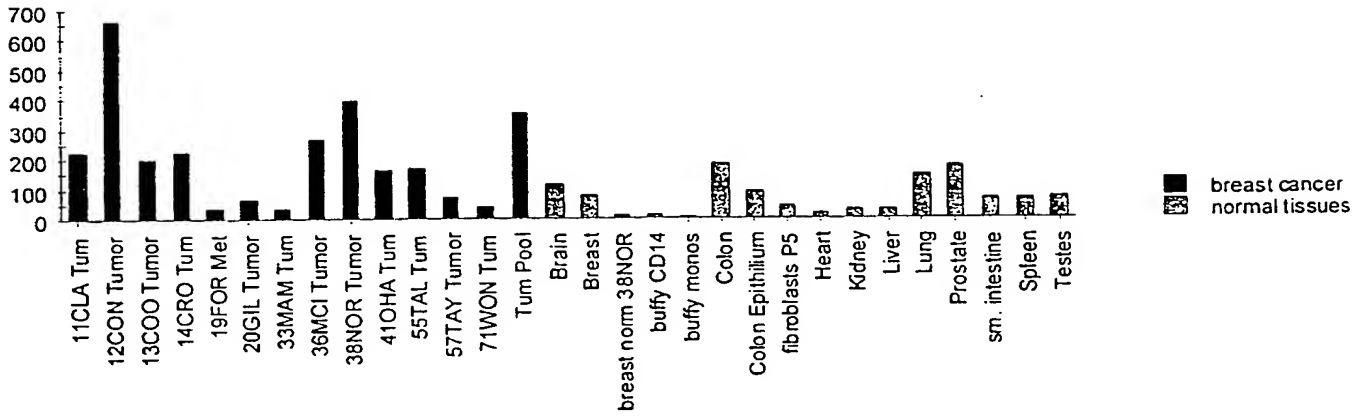
Peptide Name: BCQ8p1

Sequence: Ac-Cys-Lys-Pro-Asp-Thr-Ser-Ser-Ser-Lys-Asn-Lys
-Asp-Pro-Ile-Thr-NH_2

Peptide Name: BCQ8p2

Sequence: H-Lys-Phe-Asp-Asp-Phe-Glu-Asp-Glu-Glu-Asp
-Ile-Val-Glu-Tyr-Cys-NH_2

FIGURE 2 2



GCGCCCGGCGCTCGCAGGCCACTCTCTGCTGTCGCCCGTCCCGCGCGCTCCTCCGACCCGCTCCGCTCCGCTCCGCTCGGCCCCGCGCCG
CCCGTCAACATGATCCGCTGCGGCCTGGCCTGCGAGCGCTGCCGCTGGATCCTGCCCCTGCTCCTACTCAGCGCCATCGCCTTCGACAT
CATCGCGCTGGCCGGCCGCGGCTGGTTGCAGTCTAGCGACCACGGCCAGACGTCCTCGCTGTGGTGGAAATGCTCCCAAGAGGGCGGCG
GCAGCGGGTCCTACGAGGAGGGCTGTCAGAGCCTCATGGAGTACGCGTGGGGTAGAGCAGCGGCTGCCATGCTCTTCTGTGGCTTCATC
ATCCTGGTGATCTGTTTCATCCTCTCCTTCTTCGCCCTCTGTGGACCCCAGATGCTTGTCTTCCTGAGAGTGATTGGAGGTCTCCTTGC
CTTGGCTGCTGTGTTCCAGATCATCTCCCTGGTAATTTACCCCGTGAAGTACACCCAGACCTTCACCCTTCATGCCAACCCTGCTGTCA
CTTACATCTATAACTGGGCCTACGGCTTTGGGTGGGCAGCCACGATTATCCTGATTGGCTGTGCCTTCTTCTTCTGCTGCCTCCCCAAC
TACGAAGATGACCTTCTGGGCAATGCCAAGCCCAGGTACTTCTACACATCTGCCTAACTTGGGAATGAATGTGGGAGAAAATCGCTGCT
GCTGAGATGGACTCCAGAAGAAGAAACTGTTTCTCCAGGCGACTTTGAACCCATTTTTTGGCAGTGTTCATATTATTAAACTAGTCAAA
AATGCTAAAATAATTTGGGAGAAAATATTTTTTAAGTAGTGTTATAGTTTCATGTTTATCTTTTATTATGTTTTGTGAAGTTGTGTCTT
TTCACTAATTACCTATACTATGCCAATATTTCCTTATATCTATCCATAACATTTATACTACATTTGTAAGAGAATATGCACGTGAAACT
TAACACTTTATAAGGTAAAAATGAGGTTTCCAAGATTTAATAATCTGAYCAAGTTCTTGTTATTTCCAAATAGAATGGACTCGGTCTGT
TAAGGGCTAAGGAGAAGAGGAAGATAAGGTTAAAAGTTGTTAATGACCAAACATTCTAAAAGAAATGCAAAAAAAAAAGTTTATTTTCAA
GCCTTCGAACTATTTAAGGAAAGCAAAATCATTTCCTAAATGCATATCATTTGTGAGAATTTCTCATTAATATCCTGAATCATTCATTT
TAGCTAAGGCTTCATGTTGACTCGATATGTCATCTAGGAAAGTACTATTTCATGGTCCAAACCTGTTGCCATAGTTGGTAAGGCTTTCC
TTTAAGTGTGAAATATTTAGATGAAATTTTCTCTTTTAAAGTTCTTTATAGGGTTAGGGTGTGGGAAAATGCTATATTAATAAATCTGT
AGTGTTTTGTGTTTATATGTTCAGAACCAGAGTAGACTGGATTGAAAGATGGACTGGGTCTAATTTATCATGACTGATAGATCTGGTTA
AGTTGTGTAGTAAAGCATTAGGAGGGTCATTCTTGTCACAAAAGTGCCACTAAAACAGCCTCAGGAGAATAAATGACTTGCTTTTCTAA
ATCTCAGGTTTATCTGGGCTCTATCATATAGACAGGCTTCTGATAGTTTGCAACTGTAAGCAGAAACCTACATATAGTTAAAATCCTGG
TCTTTCTTGGTAAACAGATTTTAAATGTCTGATATAAAACATGCCACAGGAGAATTCGGGGATTTGAGTTTCTCTGAATAGCATATATA
TGATGCATCGGATAGGTCATTATGATTTTTTACCATTTCGACTTACATAATGAAAACCAATTCATTTTAAATATCAGATTATTATTTTG
TAAGTTGTGGAAAAAGCTAATTGTAGTTTTCATTATGAAGTTTTCCCAATAAACCAGGTATTCTAAACTTGAAAAAAAAAAAAAAAAAA

FIGURE 23

ATGATCCGCTGCGGCCTGGCCTGCGAGCGCTGCCGCTGGATCCTGCCCCTGCTCCTACTCAGCGCCATCGCCTTCGACATCATCGCGCT
GGCCGGCCGCGGCTGGTTGCAGTCTAGCGACCACGGCCAGACGTCCTCGCTGTGGTGGAAATGCTCCCAAGAGGGCGGCGGCAGCGGGT
CCTACGAGGAGGGCTGTCAGAGCCTCATGGAGTACGCGTGGGGTAGAGCAGCGGCTGCCATGCTCTTCTGTGGCTTCATCATCCTGGTG
ATCTGTTTCATCCTCTCCTTCTTCGCCCTCTGTGGACCCCAGATGCTTGTCTTCCTGAGAGTGATTGGAGGTCTCCTTGCCTTGGCTGC
TGTGTTCCAGATCATCTCCCTGGTAATTTACCCCGTGAAGTACACCCAGACCTTCACCCTTCATGCCAACCCTGCTGTCACTTACATCT
ATAACTGGGCCTACGGCTTTGGGTGGGCAGCCACGATTATCCTGATTGGCTGTGCCTTCTTCTTCTGCTGCCTCCCCAACTACGAAGAT
GACCTTCTGGGCAATGCCAAGCCCAGGTACTTCTACACATCTGCCTAA

FIGURE 24

```
human_BCQ5      1 MIRCGLACERCRWILPLLLLSAIAFDIIALAGRGWLQSSDHGQTSSLWWK  50
mouse_BCQ5      1 MLRCGLACERCRWILPLLLLSAIAFDIIALAGRGWLQSSNHIQTSSLWWR  50
rat_BCQ5        1                                                     0

human_BCQ5     51 CSQEGGGSGSYEEGCQSLMEYAWGRAAAAMLFCGFIILVICFILSFFALC 100
mouse_BCQ5     51 CFDEGGGSGSYDDGCQSLMEYAWGRAAAATLFCGFIILCICFILSFFALC 100
rat_BCQ5        1                         EYAWGRAAAATLFCGFIILVICFILSFFALC  31

human_BCQ5    101 GPQMLVFLRVIGGLLALAAVFQIISLVIYPVKYTQTFTLHANPAVTYIYN 150
mouse_BCQ5    101 GPQMLVFLRVIGGLLALAAIFQIISLVIYPVKYTQTFRLHDNPAVNYIYN 150
rat_BCQ5       32 GPQMLVFLRVIGGLLALAAVFQIISLVIYPVKYTQTFRLHDNPAVNYIYN  81

human_BCQ5    151 WAYGFGWAATIILIGCAFFFCCLPNYEDDLLGNAKPRYFYTSA 193
mouse_BCQ5    151 WAYGFGWAATIILIGCSFFFCCLPNYEDDLLGAAKPRYFYPPA 193
rat_BCQ5       82 WAYGFGWAATIILIGCSFFFCCLPNYEDDLLGNAKPRYFYTSA 124
```

FIGURE 25

BCQ5p1

Ac-Cys-Ser-Tyr-Ser-Ala-Pro-Ser-Pro-Ser-Thr
-Ser-Ser-Arg-Trp-Pro-NH_2

BCQ5p2

Ac-Cys-Leu-Pro-Asn-Tyr-Glu-Asp-Asp-Leu
-Leu-Gly-Asn-Ala-Lys-Pro-NH_2

BCQ5p3

Ac-Cys-Gly-Gly-Asn-Ala-Pro-Lys-Arg-Gly-Gly
-Gly-Arg-Gly-Ser-Tyr-NH_2

FIGURE 26

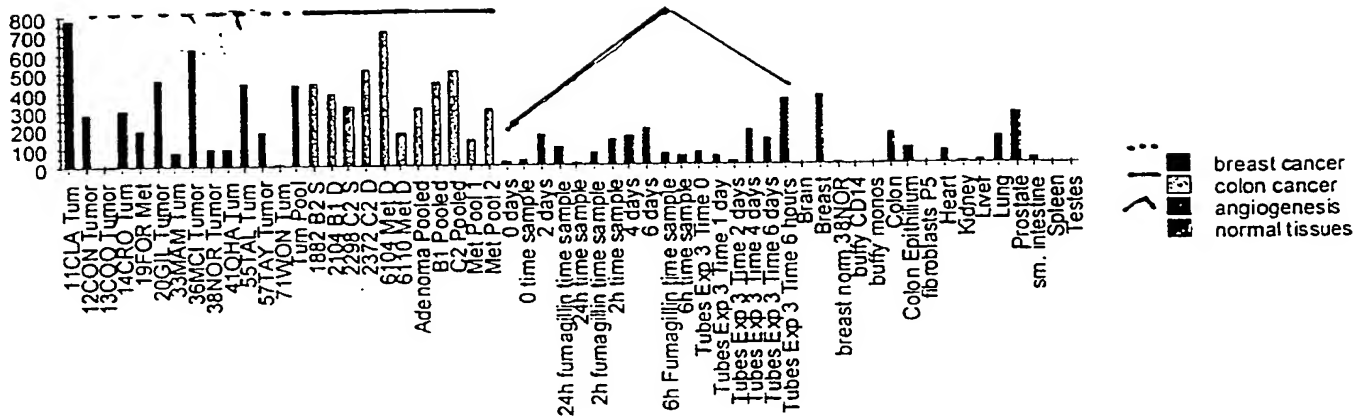


FIGURE 27

GTCACCGGAATCAAGGTGTGGCTGGAGCGCCGCTCCCCCGCCGYCAGCCCGKKGGCCGCGTCTTCGGGGGAGCCGCCTCTTCCTTWATTC
GGCKCYGACAGCGCTCGCAGGACCACTCTTGGCCGCTGCTCCTGCCCGGCGTTCCTCCGCTCCGCGCCCGCCGCCACCGACGACATGCTG
CGCTGCGGCCTGGCCTGCGAGCGCTGCAGGTGGATCCTGCCCCTGCTGCTGCTCAGCGCCATCGCCTTCGACATCATCGCGCTGGCCGGC
CGCGGCTGGCTGCAGTCTAGCAACCACATCCAGACATCGTCGCTTTGGTGGAGGTGTTTCGACGAGGGCGGCGGCAGCGGCTCCTACGAC
GATGGCTGCCAGAGCCTCATGGAGTACGCATGGGGACGAGCAGCTGCAGCCACGCTTTTCTGTGGCTTTATCATCCTGTGCATCTGCTTC
ATTCTCTCGTTCTTCGCCCTGTGTGGACCCCAGATGCTTGTTTTCCTGAGAGTCATTGGAGGCCTCCTCGCACTGGCTGCCATATTCCAG
ATCATCTCCCTGGTAATCTACCCCGTGAAGTACACACAGACCTTCAGGCTTCACGATAACCCTGCTGTTAATTACATCTATAACTGGGCC
TATGGCTTCGGATGGGCGGCCACCATCATCTTGATTGGTTGTTCCTTCTTCTTCTGCTGCCTCCCCAACTACGAGGATGACCTTTTGGGG
GCCGCCAAGCCCAGGTACTTCTATCCCCCAGCCTAATGTGGGAGGAAGAGCCTGAGAAAAGCCTGCTGCAAGATGGATCTGAGGAGGAAA
CTGTTCTCCAAGGCACAAGGAACCTACGTTTGGGCAATGTTCATATGATCAGAAATGTTAGAATAAATGCTAAAGAAAATTCTTCATAAT
TAGTGTTAAGTTTCATGTATGTCGTGTGGAGTTAAAAAGACTTGAATTCTGTTTGCTAAGTATATGCTAATTTTTCCTTATGTCAATTCT
ATACCATTTAAGCTTCATTTGTTAAAGAATATGCCTGTGAAACTTGATAAGGTAGAAATGCAGCAGCCTCTCATTTAATAATCTGATGGG
GCTTCTGTTTTTCCACATAGAATGGGTTGTTTCTGCTAAGGGCTACAGAGGAGGAAAGTCACTGGCAAAACTTCCATGACCAAATATCCT
GAAATTAGTTTGTTTTTTTTTAAAAGACCTTATTTTGAGTTTTCAGTTACATAAAGAAGCAGAAGCAGATTGGTTTCCTAAGTGAGCATC
ATTTGTGAGAATTTTTAGTCAGTGTTTTGAACAATTATTGTTTTTCTAAGCTTCATGTTGACTTTCTCTGATGCGTAGAAAAGTGTTCTA
ACGTGGCTGAGGTTAAGCCGCTGTCATTACTGAAATGCTAAGAATTTTCCTCTTTTCCCGTAGTGTAGAGGGGTAGGGTGTGGGCAGAAG
CCGTGTTAGCACATCTGTAGTATTGTGTGTGTATGCTTAGAACCAGCGTAGACCGGATGGGAGGATGGACTAGGCCTAATCCCTCCCAAC
TGGTGGATGTGAAGAGGTCAGGTAGGAAGGCACAGGAGGGTCACCACTGTCACAGCAGTGCCATGCAGACATCCTAGGAGAAGACATGGC
AGTGTTTCTTCTCAGTGCTTCTTCCCTTAACTGAGCTCTGCTCACAGACAGCTAGAATAGATTTTAACTGAAACAGAAACCTAAATGTAA
TTAAAAACCTGGTCTTCCTTGGTAAGCAGACTTAAAATATCTGTATAGTACATGCAAGTGGAAAATTTGGGAATGCGTGTCTCTGAATAC
ATACCGGAAGGGCTACTATTACCTTTTTCTTACCATTTATACTTACCTAATGGAAACGAGCTTGTTTTAACTATCAGAACACTATTTTGT
AAGGTGCTGCAAAGACAGTTGAAGTTTTCATTACCAATTTCCCCAATAAACCAGGTGTTCAAATCCTGAAAAAAAAAAGGC

FIGURE 28

ATGCTGCGCTGCGGCCTGGCCTGCGAGCGCTGCAGGTGGATCCTGCCCCTGCTGCTGCTCAGCGCCATCGCCTTCGACATCATCGCGCTG
GCCGGCCGCGGCTGGCTGCAGTCTAGCAACCACATCCAGACATCGTCGCTTTGGTGGAGGTGTTTCGACGAGGGCGGCGGCAGCGGCTCC
TACGACGATGGCTGCCAGAGCCTCATGGAGTACGCATGGGGACGAGCAGCTGCAGCCACGCTTTTCTGTGGCTTTATCATCCTGTGCATC
TGCTTCATTCTCTCGTTCTTCGCCCTGTGTGGACCCCAGATGCTTGTTTTCCTGAGAGTCATTGGAGGCCTCCTCGCACTGGCTGCCATA
TTCCAGATCATCTCCCTGGTAATCTACCCCGTGAAGTACACACAGACCTTCAGGCTTCACGATAACCCTGCTGTTAATTACATCTATAAC
TGGGCCTATGGCTTCGGATGGGCGGCCACCATCATCTTGATTGGTTGTTCCTTCTTCTTCTGCTGCCTCCCCAACTACGAGGATGACCTT
TTGGGGGCCGCCAAGCCCAGGTACTTCTATCCCCCAGCCTAA

FIGURE 29

GAATACGCCTGGGGCCGAGCAGCTGCTGCCACTCTCTTCTGTGGATTCATCATCCTGGTCATCTGCTTCATCCTCTCGTTCTTCGCCCTG
TGTGGACCCCAGATGCTTGTTTTCCTGAGAGTGATTGGAGGCCTTCTCGCACTGGCTGCTGTATTCCAGATCATCTCCCTGGTTATCTAT
CCCGTGAAGTACACACAAACCTTCAGGCTTCATGATAATCCCGCTGTTAATTACATCTACAACTGGGCCTATGGCTTCGGATGGGCAGCC
ACGATCATCTTGATTGGTTGCTCTTTCTTCTTCTGCTGCCTCCCCAACTACGAGGATGACCTTCTGGGCAATGCAAAGCCCAGGTACTTC
TATACATCTGCCTAATGTGGAGGGAGATCCTGAGAAAAGCCTGCTGCAAGATGCATGTGAGGAGGAAAGTGTTCTCCAAGGAGCAAAGAA
CCTATGTTTGGGCAGTGTTCATATGAGTGGAAATGCTAGAATAAATGCTAAAGAAAATTCTTCATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

GAATACGCCTGGGGCCGAGCAGCTGCTGCCACTCTCTTCTGTGGATTCATCATCCTGGTCATCTGCTTCATCCTCTCGTTCTTCGCCCTG
TGTGGACCCCAGATGCTTGTTTTCCTGAGAGTGATTGGAGGCCTTCTCGCACTGGCTGCTGTATTCCAGATCATCTCCCTGGTTATCTAT
CCCGTGAAGTACACACAAACCTTCAGGCTTCATGATAATCCCGCTGTTAATTACATCTACAACTGGGCCTATGGCTTCGGATGGGCAGCC
ACGATCATCTTGATTGGTTGCTCTTTCTTCTTCTGCTGCCTCCCCAACTACGAGGATGACCTTCTGGGCAATGCAAAGCCCAGGTACTTC
TATACATCTGCCTAA

FIGURE 31

FIGURE 32

CTTTGAAGCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGTACTCTTGGGAG
TTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTGACACGTATCCAGCTACTGGTCCTGCTGAT
GATGAAGCCCCTGATGCTGAAACCACTGCTGCTGCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGC
TTCTACCACTGCTCGTAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCCTGAG
ATGGAATCAGCTTGAGTCTTCTGCAATTGGGTCACAACTATTCATGCTTCCTGTGATTTCATCCAACTACTTACCTTGCC
TACGATATCCCCTTTATCTCTAATCAGTTTATTTTCTTTCAAATAAAAAATAACTATGAGCGAGCTAACAT

FIGURE 33

ATGAAGTTCTTAGCAGTCCTGGTACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCC
AGCTGACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCTGCAACCACTGCGA
CCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCGTAAAGACATTCCAGTTTTACCCAAATGGGTT
GGGGATCTCCCGAATGGTAGAGTGTGTCCCTGA

FIGURE 34

MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTTATTAASTTARKDIPVLPKWV
GDLPNGRVCP.

FIGURE 35

H-Gln-Asn-Pro-Thr-Thr-Ala-Ala-Pro-Ala-Asp-Thr-Tyr-Pro-Ala-Cys-NH_2

Ac-Leu-Pro-Lys-Trp-Val-Gly-Asp-Leu-Pro-Asn-Gly-Arg-Val-Cys-Pro-OH

FIGURE 36

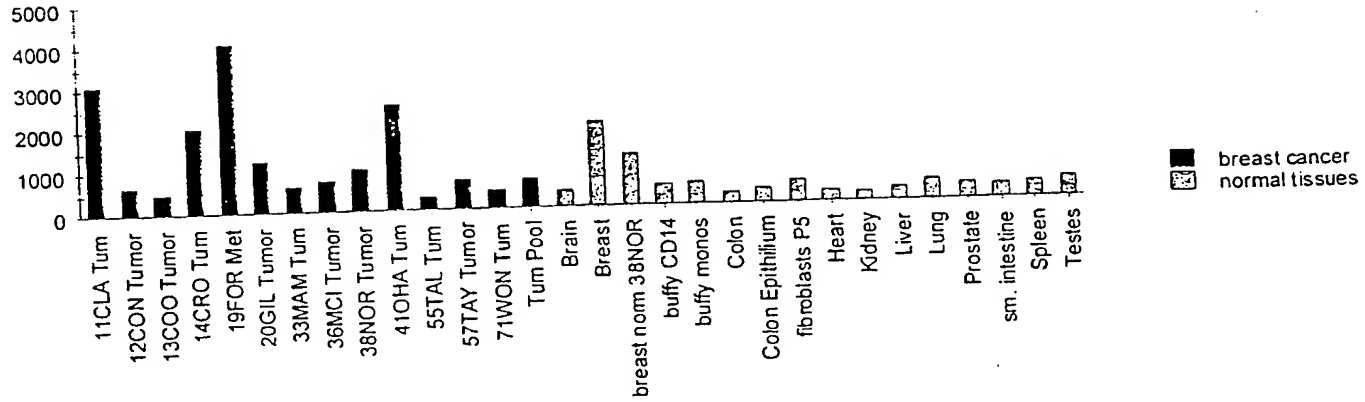


FIGURE 37

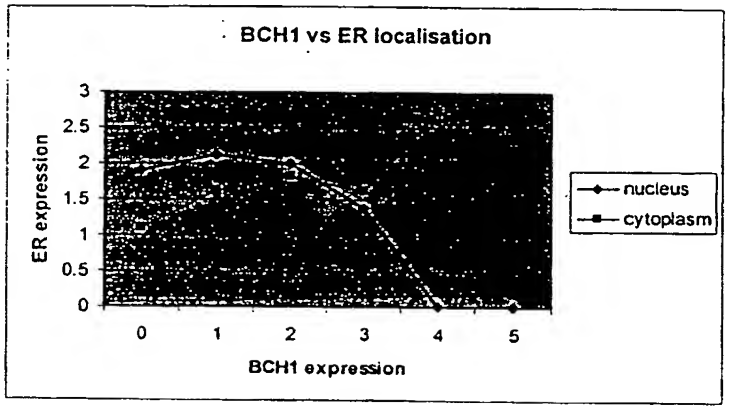


FIGURE 38A FIGURE 38B

FIGURE 39A FIGURE 39B

FIGURE 40A

FIGURE 40B

FIGURE 41A

FIGURE 41B

FIGURE 4 2

GGAGTTTTCTGGAGCTGTTGCAATGTGTATGCTGGTGAAATCTACTTGAGCATTAAGCAGTATCTCCCAGC
ATTGTTAGCTACTGAGTGGCACATCTTCAGTACGCATGATTCGTGGGGGACTCAGGCAGAGGTAAAAGTGT
GAAACTTTTCAGCATTACCTAAGAAGCAAAGGCTCAATTTTGGCTGCTTCATTCTTATCTCTTCTGCCACA
GTTCTAACGTGCCTGATCTACTGAGACCAAGG[redacted]ACCAATGACTCAGAAGGGAAAATGGGATTTAAACAC
CCAAAGATCATGGGGAATTTCAGAGGTCATGCCCTCCCTGGAACCTTCTTTTTTATTATTGGTCTTTGGTG
GTGTACAAAGAGTATTCTGAAGTATATCTGCAAAAAGCAAAAGCGAACCTGCTATCTTGGTTCCAAAACAT
TATTCTATCGATTGGAAATTTTGGAGGGAATTACAATAGTTGGCATGGCTTTAACTGGCATGGCTGGGGAG
CAGTTTATTCCTGGAGGGCCCCATCTGATGTTATATGACTATAAACAAGGTCACTGGAATCAACTCCTGGG
CTGGCATCATTTCACCATGTATTTCTTCTTTGGGCTGTTGGGTGTGGCAGATATCTTATGTTTCACCATCA
GTTCACTTCCTGTGTCCTTAACCAAGTTAATGTTGTCAAATGCCTTATTTGTGGAGGCCTTTATCTTCTAC
AACCACACTCATGGCCGGGAAATGCTGGACATCTTTGTGCACCAGCTGCTGGTTTTGGTCGTCTTTCTGAC
AGGCCTCGTTGCCTTCCTAGAGTTCCTTGTTCGGAACAATGTACTTCTGGAGCTATTGCGGTCAAGTCTCA
TTCTGCTTCAGGGGAGCTGGTTCTTTCAGATTGGATTTGTCCTGTATCCCCCCAGTGGAGGTCCTGCATGG
GATCTGATGGATCATGAAAATATTTTGTTTCTCACCATATGCTTTTGTTGGCATTATGCAGTAACCATTGT
CATCGTTGGAATGAATTATGCTTTCATTACCTGGTTGGTTAAATCTAGACTTAAGAGGCTCTGCTCCTCAG
AAGTTGAAAAAGACTTCTGTGCTGAACGAGAACAAGAATCAGAAGAAGAAATG[redacted]CTTTGATGAGCTTCC
AGTTTTTCTAGATAAACCTTTTCTTTTTTACATTGTTCTTGGTTTTGTTTCTCGATCTTTTGTTTGGAGAA
CAGCTGGCTAAGGATGACTCTAAGTGTACTGTTTGCATTTCCAATTTGGTTAAAGTATTTGAATTTAAATA
TTTTCTTTTTAGCTTTGAAAATATTTTGGGTGATACTTTCATTTTGCACATCATGCACATCATGGTATTCA
GGGGCTAGAGTGATTTTTTTCCAGATTATCTAAAGTTGGATGCCCACACTATGAAAGAAATATTTGTTTTA
TTTGCCTTATAGATATGCTCAAGGTTACTGGGCTTGCTACTATTTGTAACTCCTTGACCATGGAATTATAC
TTGTTTATCTTGTTGCTGCAATGAGAAATAAATGAATGTATGTATTTTGGTGCAGAAAAAAAAA

FIGURE 4 3

MTNDSEGKMGFKHPKIMGNFRGHALPGTFFFIIGLWWCTKSILKYICKKQKRTCYLGSKTLFYRLEILEGI
TIVGMALTGMAGEQFIPGGPHLMLYDYKQGHWNQLLGWHHFTMYFFFGLLGVADILCFTISSLPVSLTKLM
LSNALFVEAFIFYNHTHGREMLDIFVHQLLVLVVFLTGLVAFLEFLVRNNVLLELLRSSLILLQGSWFFQI
GFVLYPPSGGPAWDLMDHENILFLTICFCWHYAVTIVIVGMNYAFITWLVKSRLKRLCSSEVGLLKNAERE
QESEEEM.

BCN1p1

Ac-Tyr-Pro-Pro-Ser-Gly-Gly-Pro-Ala-Trp-
Asp-Leu-Met-Asp-His-Cys-NH_2

BCN1p2

Ac-Cys-Leu-Lys-Asn-Ala-Glu-Arg-Glu-Gln-Glu-Ser
-Glu-Glu-Glu-Met-OH

FIGURE 44

FIGURE 15

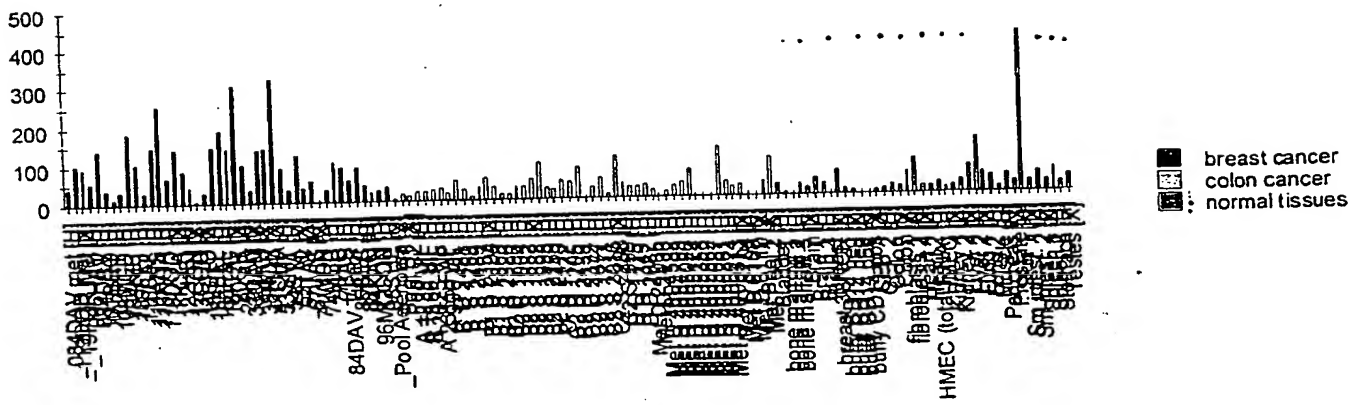


FIGURE 46A

TTCCTCCGCGAAGGCTCCTTTGATATTAATAGTGTTGGTGTCTTGAAACTGACGTAATGCGCGG
AGACTGAGGTCCTGACAAGCGATAACATTTCTGATAAAGACCCGATCTTACTGCAATCTCTAG
CGTCCTCTTTTTTGGTGCTGCTGGTTTCTCCAGACCTCGCGTCCTCTCGATTGCTCTCTCGCCTT
CCTATTTCTTTTTTTTTTTTTTTAAACAAAAAACAACACCCCCTCCCCTCTCCCACCCGGCACCG
GGCACATCCTTGCTCTATTTCCTTTCTCTTTCTCTCTCTCTCTCTCTCTCTCTTTTTTAATAAG
GGTGGGGGAGGGAAAGGGGGGGGATGCAGGAAAGACCTTTTTCTCTCCCCCCCGCAATAATC
CAAGATCAACTCTGCAAACAACAGAAGACGGTTCATGGCTTTGGCCGCCGCGCCACCATCTTT
CGGGCTGCCGAGGGTGTTCTTGACGATTAATCAACAGATGTACAGATCAGCTCTCAAAATGTC
TTCTGTGTCTTCTGAGCGTCTTCTAAGACAATTGCATTAGCCTCCTGCTAGTTGACTAATAGAA
TTAATAATTGTAAAAAGCACTCTAAAGCCACATGCCTTATGAAGTCAATGCTGGGTATGATTT
TACAAATAAAAGTCCGGAAAAAGAACCCCCCTCTGAGAAACGTTGCAAGTGAAGGCGAGGGCC
AGATCCTGGAGCCTATAGGTACAGAAAGCAAGGTATCTGGAAAGAACAAAGAATTTTCTGCA
GATCAGATGTCAGAAAATACGGATCAGAGTGATGCTGCAGAACTAAATCATAAGGAGGAACA
TAGCTTGCATGTTCAAGATCCATCTTCTAGCAGTAAGAAGGACTTGAAAAGCGCAGTTCTGAG
TGAGAAGGCTGGCTTCAATTATGAAAGCCCCAGTAAGGGAGGAAACTTTCCCTCCTTTCCGCA
TGATGAGGTGACAGACAGAAATATGTTGGCTTTCTCATCTCCAGCTGCTGGGGGAGTCTGTGA
GCCCTTGAAGTCTCCGCAAAGAGCAGAGGCAGATGACCCTCAAGATATGGCCTGCACCCCCTC
AGGGGACTCACTGGAGACAAAGGAAGATCAGAAGATGTCACCAAAGGCTACAGAGGAAACA
GGGCAAGCACAGAGTGGTCAAGCCAATTGTCAAGGTTTGAGCCCAGTTTCAGTGGCCTCAAA
AAACCCACAAGTGCCTTCAGATGGGGGTGTAAGACTGAATAAATCCAAAACTGACTTACTGG
TGAATGACAACCCAGACCCGGCACCTCTGTCTCCAGAGCTTCAGGACTTTAAATGCAATATCT
GTGGATATGGTTACTACGGCAACGACCCCACAGATCTGATTAAGCACTTCCGAAAGTATCACT
TAGGACTGCATAACCGCACCAGGCAAGATGCTGAGCTGGACAGCAAAATCTTGGCCCTTCAT
AACATGGTGCAGTTCAGCCATTCCAAAGACTTCCAGAAGGTCAACCGTTCTGTGTTTTCTGGT
GTGCTGCAGGACATCAATTCTTCAAGGCCTGTTTTACTAAATGGGACCTATGATGTGCAGGTG
ACTTCAGGTGGAACATTCATTGGCATTGGACGGAAAACACCAGATTGCCAAGGGAACACCAA
GTATTTCCGCTGTAAATTCTGCAATTTCACTTATATGGGCAACTCATCCACCGAATTAGAACAA
CATTTTCTTCAGACTCACCCAAACAAAATAAAAGCTTCTCTCCCCTCCTCTGAGGTTGCAAAAC
CTTCAGAGAAAAACTCTAACAAGTCCATCCCTGCACTTCAATCCAGTGATTCTGGAGACTTGG
GAAAATGGCAGGACAAGATAACAGTCAAAGCAGGAGATGACACTCCTGTTGGGTACTCAGTG
CCCATAAAGCCCCTCGATTCCTCTAGACAAAATGGTACAGAGGCCACCAGTTACTACTGGTGT
AAATTTTGTAGTTTCAGCTGTGAGTCATCTAGCTCACTTAAACTGCTAGAACATTATGGCAAG
CAGCACGGAGCAGTGCAGTCAGGCGGCCTTAATCCAGAGTTAAATGATAAGCTTTCCAGGGG
CTCTGTCATTAATCAGAATGATCTAGCCAAAAGTTCAGAAGGAGAGACAATGACCAAGACAG
ACAAGAGCTCGAGTGGGGCTAAAAAGAAGGACTTCTCCAGCAAGGGAGCCGAGGATAATATG
GTAACGAGCTATAATTGTCAGTTCTGTGACTTCCGATATTCCAAAAGCCATGGCCCTGATGTA
ATTGTAGTGGGGCCACTTCTCCGTCATTATCAACAGCTCCATAACATTCACAAGTGTACCATTA
AACACTGTCCATTCTGTCCCAGAGGACTTTGCAGCCCAGAAAAGCACCTTGGAGAAATTACTT
ATCCGTTTGCTTGTAGAAAAAGTAATTGTTCCCACTGTGCACTCTTGCTTCTGCACTTGTCTCC
TGGGGCGGCTGGAAGCTCGCGAGTCAAACATCAGTGCCATCAGTGTTCATTCACCACCCCTGA
CGTAGATGTACTCCTCTTTCACTATGAAAGTGTGCATGAGTCCCAAGCATCGGATGTCAAACA
AGAAGCAAATCACCTGCAAGGATCGGATGGGCAGCAGTCTGTCAAGGAAAGCAAAGAACACT
CATGTACCAAATGTGATTTTATTACCCAAGTGGAAGAAGAGATTTCCCGACACTACAGGAGAG
CACACAGCTGCTACAAATGCCGTCAGTGCAGTTTTACAGCTGCCGATACTCAGTCACTACTGG
AGCACTTCAACACTGTTCACTGCCAGGAACAGGACATCACTACAGCCAACGGCGAAGAGGAC
GGTCATGCCATATCCACCATCAAAGAGGAGCCCAAAATTGACTTCAGGGTCTACAATCTGCTA
ACTCCAGACTCTAAAATGGGAGAGCCAGTTTCTGAGAGTGTGGTGAAGAGAGAGAAGCTGGA
AGAGAAGGACGGGCTCAAAGAGAAAGTTTGGACCGAGAGTTCCAGTGATGACCTTCGCAATG
TGACTTGGAGAGGGGCAGACATCCTGCGGGGGAGTCCGTCATACACCCAAGCAAGCCTGGGG
CTGCTGACGCCTGTGTCTGGCACCCAAGAGCAGACAAAGACTCTAAGGGATAGTCCCAATGT
GGAGGCCGCCCATCTGGCGCGACCTATTTATGGCTTGGCTGTGGAAACCAAGGGATTCCTGCA

FIGURE 46B

GGGGGCGCCAGCTGGCGGAGAGAAGTCTGGGGCCCTCCCCCAGCAGTATCCTGCATCGGGAG
AAAACAAGTCCAAGGATGAATCCCAGTCCCTGTTACGGAGGCGTAGAGGCTCCGGTGTTTTTT
GTGCCAATTGCCTGACCACAAAGACCTCTCTCTGGCGAAAGAATGCAAATGGCGGATATGTAT
GCAACGCGTGTGGCCTCTACCAGAAGCTTCACTCGACTCCCAGGCCTTTAAACATCATTAAAC
AAAACAACGGTGAGCAGATTATTAGGAGGAGAACAAGAAAGCGCCTTAACCCAGAGGCACTT
CAGGCTGAGCAGCTCAACAAACAGCAGAGGGGCAGCAATGAGGAGCAAGTCAATGGAAGCC
CGTTAGAGAGGAGGTCAGAAGATCATCTAACTGAAAGTCACCAGAGAGAAATTCCACTCCCC
AGCCTAAGTAAATACGAAGCCCAGGGTTCATTGACTAAAAGCCATTCTGCTCAGCAGCCAGTC
CTGGTCAGCCAAACTTTGGATATTCACAAAAGGATGCAACCTTTGCACATTCAGATAAAAAGT
CCTCAGGAAAGTACTGGAGATCCAGGAAATAGTTCATCCGTATCTGAAGGGAAAGGAAGTTC
TGAGAGAGGCAGTCCTATAGAAAAGTACATGAGACCTGCGAAACACCCAAATTATTCACCAC
CAGGCAGCCCTATTGAAAAGTACCAGTACCCACTTTTTGGACTTCCCTTTGTACATAATGACTT
CCAGAGTGAAGCTGATTGGCTGCGGTTCTGGAGTAAATATAAGCTCTCCGTTCCTGGGAATCC
GCACTACTTGAGTCACGTGCCTGGCCTACCAAATCCTTGCCAAAACTATGTGCCTTATCCCACC
TTCAATCTGCCTCCTCATTTTTCAGCTGTTGGATCAGACAATGACATTCCTCTAGATTTGGCGA
TCAAGCATTCCAGACCTGGGCCAACTGCAAACGGTGCCTCCAAGGAGAAAACGAAGGCACCA
CCAAATGTAAAAAAATGAAGGTCCCTTGAATGTAGTAAAAACAGAGAAAGTTGATAGAAGTAC
TCAAGATGAACTTTCAACAAAATGTGTGCACTGTGGCATTGTCTTTCTGGATGAAGTGATGTA
TGCTTTGCATATGAGTTGCCATGGTGACAGTGGACCTTTCCAGTGCAGCATATGCCAGCATCTT
TGCACGGACAAATATGACTTCACAACACATATCCAGAGGGGCCTGCATAGGAACAATGCACA
AGTGGAAAAAAAATGGAAAACCTAAAGAGTAAAAACCTTAGCACTTAGCACAATTAAATAGAA
ATAGGTTTTCTTGATGGGAATTCAATAGCTTGTAATGTCTTATGAAGACCTATTAAAAAAATA
CTTCATAGAGCCTGCCTTATCCAACATGAAATTCCCTTCTTTTGTTATTCTTTCTTTTGATGAGT
AGGTTACCAAGATTAAAAAGTGAGATAAATGGTCAATGAGAAAGAATGGAAGATGGTAAAC
AATCACTTTTTAAAACCTGTTAAGTCAAAACCATCTTGGCTAATATGTACTGGGGAAATAATC
CATAAGAGATATCACCAGACTAGAATTAATATATTTATAAAGAAAGAGACCAAAACTGTCTA
GAATTTGAAAGGGTTTACATATTATTATACTAAAGCAGTACTGGACTGGCCATTGGACCATTT
GTTCCAAAACCCATAAATTGTTGCCTAAATTTATAATGATCATGAAACCCTAGGCAGAGGAGG
AGAAATTGAAGGTCCAGGGCAATGAAAGAAAAATGGCGCCCTCTCAATTTAGTCTTCTCTCAT
TGGCCATGTTTCAGATTTTGACCTAGAAATGCGAGCTGTGGTTAGGCTTGGTTAGAGTGCAGC
AAGCAACATGACAGATGGTGGCACGCTGTTTTTACCCAGCCCTGCCTGTACATACACATGCAC
ACCCTCTCTGATATTTTTGTCCTTTAGATGTTCAAATACTCAGTAGTCCTTTTGTTTGCGGTTTA
GATTCATTTTGTCCACACATGTACCCATTTTAAAAAACAATGTCCTCGATGCTTCTGTAGTGAT
TTCATTTTAGCCAGGTATTTCTTTCTTGTGTGTGATGAACCAGTATGGATTTGCTTTTCTAAGCC
TCCTGTTGGTTACTAATCTCACTTGGCACATTATAACTAAAGGAATCCCCTCAATTCAAAAGC
ATAGATGGATACAAATGTCAGACCGTGGGTTTAATTTGTTTAGAACACATGGCATTTCTTCAC
AAGGTAACCTGCTGTATTTATTTATTTTCTTTTGGTTAAATATAATTTCCAAACTTTGTGGTCAG
GCAGCGTCTAAGGTTACGTTACCACAGACTGACAGTTGGTATATGTACCAGCCAATCCCTTCA
TTAAATGTATACAGATTTAGTTAAGTAGCATTAAATAGGATTCTTAGAAGTATGTCCTCATAG
AACTTTTAATACTTAAGGCTTTGTAAAAACTATCCATGAAGGGAAAGCTCCTCAGCATAACTG
CTCAGGGAAATAGGGCTAAATAACTGAACATTAAATAATTGGTTAAAGGTGCTGTTAGTCGA
GCCTCAATGCTTGCTACAAGGATGTATGTACAAGGACTGACTTTAATAATTTGCATTATATTGT
CCCAACCAGTAGTTTATTTTTTGCCACGGAGATGTAGAAGATATTACAAGCTACTGGATGCAC
TGTCAGATTAACTTATTTCATTAAAGAAGTTGGGAGAACAAATAGGAAAAAAAAAAACTTATTT
TTCTAGTAAATATTAATGTATTACATTTCAAATAATGGTGCCTGACATATTGAATAATTATTTT
CTACAGTGTACGTATGCAACAAAGATATTCCATCATGCATTAGAGTCAGTTCTGGCTCTGCCT
AGCTGTTTACATTTGCAAATGTAGCAAACAAGGTAATGAAGCAACTATTTCTATTGCAGTAGA
TATCCTTTTGTGTGTGTGTGTGTGCATTAAAGTTGTAAACGGTAACATGAAACAAATGAAAGT
TCTTGCTATAATGGTATGGAAAACAAGAAGGAAATGAAAATATTTTTATGCCTACTTAGGAAA
AAAAGGGTAGCACTTATTCATTCCAAGTACTTTTTTTTTTTTAATTTTTAAGCTCTTAACTCACA
TTGTTATGCTTAAGATGATAAACATATATCCTCTTTTTATTGCTTTGTCTATGTTTCATATGAAA
CATTTCAGAAATTATTTTGATAAGTGTTGCTGGAATCTGCAACGCTGATTTTTTTTTGCATTCT
GTAGTCGCATTTGCACTCCATTTTTACATTAATTCGCAGTTGCTTTGTATCATTGTTTTGTTTGG
GTTTTGTTTCTTTTTCACAGTGCCGGGTCTTCGTTTCTTAAAGTTGGATGGCAGGTAGAGTTCA
ACCAGTTCGTGACTGTTGTAGCGAATGAAGTTAAAAAAAATGTCTTTCTGATGTTGTGTTGTCAT
TTTCATTTTTGCATTTTTTTGTTTGCATATTAAAAAAAGAGAAAAGAGAAAGCAAGAGACAGA

FIGURE 46C

AATCAGGACTAAGTCCTCTGCTTCAGTTTCATTGTTAACGGGCCTTATTCTGATCTCACCTGTC
GCGTAGCTCTAATATTCACATAAACTGAAATAAAGAAGTGGAATGAGGAGCTTTGACATTCA
AATTATGTGATGTAATTTATCTTCCTTAGGAATTTTGATGGATGCATCTCAAAATGTATAGCCA
GACTTGAGAGGTGACAATTAAAGATCTAAAAAAAGAGAGGAGATTCCCCCAAACAACAATATT
TAATTTTCTTAGTAAAAAAGAATAACAGAATGCATCGTGGCAATCCTTAAGCAACATTATCTAT
GTGGACTGCTTAAATCAGCAAAACACCAGAAGTTTGGTTAACTTGGGCAATATGACAAGTATT
ACTTTTTGGGCAAAACTACTCATTAAGCAATTTCTCTAGTGTGTCGGACACAAATAGGTTCTTT
ATTTTTGGCATGTATGCCTTTTTATTTTCATTCAATTTTTTTTTTTTCTCAGACAGACATAGTAG
TATCAACTAGCATTGGAAAATACATATCACTATTCTTGGAATATTTATGGTCAGTCTACTTTTT
AGTAAAATATTTTTGGATAGCGTTGACACGATAGATCTTATTCCATACTTCTTTATTATTGATA
ATTTTATTTTCATTTTTTGCTTTCATTATTATACATATTTTGGTGGAGAAGAGGTTGGGCTTTTT
TGAAAGAGACAAAAATTTATTATAACACTAAACACTCCTTTTTTGACATATTAAAGCCTTTATT
CCATCTCTCAAGATATATTATAAAATTTATTTTTTTAATTTAAGATTTCTGAATTATTTTATCTT
AAATTGTGATTTTAAACGAGCTATTATGGTACGGAACTTTTTTTAATGAGGAATTTCATGATGA
TTTAGGAATTTTCTCTCTTGGAAAAGGCTTCCCCTGTGATGAAAATGATGTGCCAGCTAAAATT
GTGTGCCATTTAAAAACTGAAAATATTTTAAAATTATTTGTCTATATTCTAAATTGAGCTTTGG
ATCAAACTTTAGGCCAGGACCAGCTCATGCGTTCTCATTCTTCCTTTTCTCACTCTTTCTCTCAT
CACTCACCTCTGTATTCATTCTGTTGTTTGGGATAGAAAAATCATAAAGAGCCAACCCATCTC
AGAACGTTGTGGATTGAGAGAGACACTACATGACTCCAAGTATATGAGAAAAGGACAGAGCT
CTAATTGATAACTCTGTAGTTCAAAAGGAAAAGAGTATGCCCAATTCTCTCTACATGACATAT
TGAGATTTTTTTTAATCAACTTTTAAGATAGTGATGTTCTGTTCTAAACTGTTCTGTTTTAGTGA
AGGTAGATTTTTATAAAACAAGCATGGGGATTCTTTTCTAAGGTAATATTAATGAGAAGGGAA
AAAAGTATCTTTAACAGCTCTTTGTTGAAGCCTGTGGTAGCACATTATGTTTATAATTGCACAT
GTGCACATAATCTATTATGATCCAATGCAAATACAGCTCCAAAAATATTAAATGTATATATAT
TTTAAAATGCCTGAGGAAATACATTTTTCTTAATAAACTGAAGAGTCTCAGTATGGCTATTAA
AATAATTATTAGCCTCCTGTTGTGTGGCTGCAAAACATCACAAAGTGACCGGTCTTGAGACCT
GTGAACTGCTGCCCTGTTTAGTAAATAAAATTAATGCATTTCTAGAGGGGGAATATCTGCCAT
CCAGTGGTGGAAATGTGGAGTAAAGAAGCTGGTGGTCTGCTTCTGTGCTGTATGCCAGCCTTT
TGCCTTAAGTTGAGAGGAGGTCAACTTTAGCTACTGTCTTTGGTTTGAGAGCCATGGCAAAAA
AAAAAAAAGAAAAAAAGATCAAGTCGTCTTTGGTGAGCCAGTAAGGTGAAAGCTTGCTGACT
GTCCAAGGCACAAGAGAAAATTGAGGAATTGAAATGCAACCTGAGTATCAAACTAAATATTC
TAATCAAAGGTAGGTACTGTTAGGTGGAATTCTATCAGCAGGCAACTGCAAATGAGAAGAAG
ATAGAAGGACGCCCGTCGGGACTTTGGAGGGCATTGTTATTTTCCCAAAGAAAGACGGCCAA
GGGCAGAGGCATGGATTCTTTGCAGAGCACTTCCTTTTGGTTTTTCAGTACTGTTTCATAGACA
GTGGGCTCACATGTTCCTGATAGTGCTGCAGTTGCTTAGAAAGCATCCCAGTTAATTGCAGTA
ATTAGAACTTCTGGAATATGCTAGGGCAGAAGTATGTCAAGTATGTCACATGAAGAAAATGT
GAAATTCAAGAGTAATCCACACGTGAGAAACTAGACAATGTACATTCATGTGTTCTCTTGAAA
GGAAAGGGAGAGCTGTAAGCTTCACTCTGTCCTACACCGGAGAAAAGCAGGAATAACTTTAC
CGTGGAAATAATGTTTAGCTTTTATCAGAGAAAATTGTCCTTCTAGAGCATAGAGTCCCAAAA
CTCAATTCTGGTTTTCCCCTGTTTTTTTTTTTTTTTTTTTTTCCCAACATATGAACTGCAGCAT
ATCACTTTTTCTTTTTGTGCCTCAGGTTCCTCASCTGTAAAATTGAAAAATATATGTATTA
ATAATATTATTAATAATAATAATGGTAATGTAGTACTTGTTTGTAAAGCACTTTGAGATC
CTTGGTTGAAAGGCACCATAGGAGTGCCAAGTATTATTATGTGGCCAAGGGGGTTATTT
AAACTGTCAGTTCCCAAAGGCCAGGAAAGGTTGGGGTCATTTTTCTTAAAGACGAGCTG
TAAATATCAACTAGGCAGCCAATAGTGTTGACTATGAAGATGCAAAACTATTACTAGGCT
GATAAAATCATAGTTTCTTAATGGCTACCAATAAGGCAAATATCACAATAATAAACGCCA
AATTCCTTAGGGCGGACTATTTGACAACCACATGGAAAACTTTGGGGGAGGCATGAGGG
GGGAACATCTCAAAATGCCAATGTAAAATTTAACTTACAGCAATATTCACCAGCAGAAAA
TGTCTTTCATATGGAATGATTTCATGTTGCTAAGAAAAAGAATTCAATTTGTAGTCCTGA
TTTGAATACTAGAATGTTGGCTATAATAGTTCTGTTCTTACAACACATGAAATTTTTTCGT
TTTATTTTATTTTGTTTTCATAGTGCATGTTCATTTCTACTCACAAACATGTTCTTGGTGT
ATTTCTTATGCAAACAATCTTCAGGCAGCAAAGATGTCTGTTACATCTAAACTTGAATAA
TAAAGTTTTACCACCAGTTACACATAACGGCGTTGGTATGGTTTATATGGATTCACTTTC
ATCCTTCTAGGCAATAGGGAAATACAGATCATTGTAATATATATATATATATATACAGGC
TCTGCTGAANTGAAATGGTGAAATCAAATCACCATTCTAAAAAATTATTACTTATATTGA
TAAAGCCTGGANTCTCTCAACTTGTTTTGCTTTGCTTTTTTTCTTTAACCAATCAATCTCT

TACTGATAGATTTTGTGTAAAAAGATATATACTAGTTTCTTCAGAAAGATTAACAATAAA
AATTGTGTTTATTTCAAAAAAAAAAA

FIGURE 46D

MVRKKNPPLRNVASEGEGQILEPIGTESKVSGKNKEFSADQMSENTDQSDAAELNHKEEHSLHVQ
DPSSSSKKDLKSAVLSEKAGFNYESPSKGGNFPSFPHDEVTDRNMLAFSSPAAGGVCEPLKSPQRA
EADDPQDMACTPSGDSLETKEDQKMSPKATEETGQAQSGQANCQGLSPVSVASKNPQVPSDGGV
RLNKSKTDLLVNDNPDPAPLSPELQDFKCNICGYGYYGNDPTDLIKHFRKYHLGLHNRTRQDAEL
DSKILALHNMVQFSHSKDFQKVNRSVFSGVLQDINSSRPVLLNGTYDVQVTSGGTFIGIGRKTPDC
QGNTKYFRCKFCNFTYMGNSSTELEQHFLQTHPNKIKASLPSSEVAKPSEKNSNKSIPALQSSDSGD
LGKWQDKITVKAGDDTPVGYSVPIKPLDSSRQNGTEATSYYWCKFCSFSCESSSSLKLLEHYGKQ
HGAVQSGGLNPELNDKLSRGSVINQNDLAKSSEGETMTKTDKSSSGAKKKDFSSKGAEDNMVTS
YNCQFCDFRYSKSHGPDVIVVGPLLRHYQQLHNIHKCTIKHCPFCPRGLCSPEKHLGEITYPFACRK
SNCSHCALLLLHLSPGAAGSSRVKHQCHQCSFTTPDVDVLLFHYESVHESQASDVKQEANHLQGS
DGQQSVKESKEHSCTKCDFITQVEEEISRHYRRAHSCYKCRQCSFTAADTQSLLEHFNTVHCQEQD
ITTANGEEDGHAISTIKEEPKIDFRVYNLLTPDSKMGEPVSESVVKREKLEEKDGLKEKVWTESSSD
DLRNVTWRGADILRGSPSYTQASLGLLTPVSGTQEQTKTLRDSPNVEAAHLARPIYGLAVETKGFL
QGAPAGGEKSGALPQQYPASGENKSKDESQSLLRRRRGSGVFCANCLTTKTSLWRKNANGGYVC
NACGLYQKLHSTPRPLNIIKQNNGEQIIRRRTRKRLNPEALQAEQLNKQQRGSNEEQVNGSPLERR
SEDHLTESHQREIPLPSLSKYEAQGSLTKSHSAQQPVLVSQTLDIHKRMQPLHIQIKSPQESTGDPGN
SSSVSEGKGSSERGSPIEKYMRPAKHPNYSPPGSPIEKYQYPLFGLPFVHNDFQSEADWLRFWSKY
KLSVPGNPHYLSHVPGLPNPCQNYVPYPTFNLPPHFSAVGSDNDIPLDLAIKHSRPGPTANGASKEK
TKAPPNVKNEGPLNVVKTEKVDRSTQDELSTKCVHCGIVFLDEVMYALHMSCHGDSGPFQCSICQ
HLCTDKYDFTTHIQRGLHRNNAQVEKNGKPKE

FIGURE 47

FIGURE 48

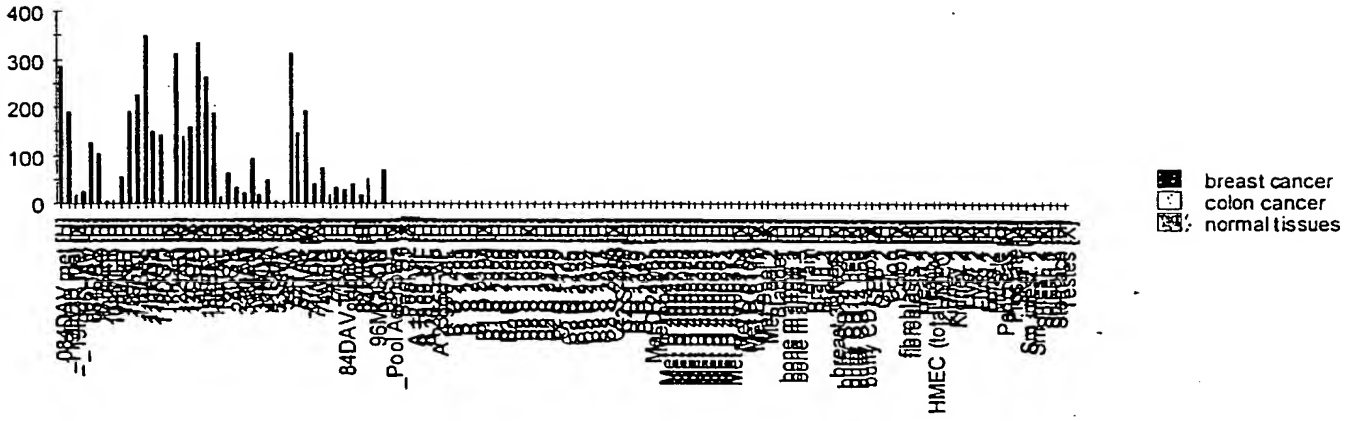


FIGURE 49A

ACTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGTGGCCACCCACCATCATCTAAAGAAGA
TAAACTTGGCAAATGACATGCAGGTTCTTCAAGGCAGAATAATTGCAGAAAATCTTCAAAGG
ACCCTATCTGCAGATGTTCTGAATACCTCTGAGAATAGAGATTGATTATTCAACCAGGATACC
TAATTCAAGAACTCCAGAAATCAGGAGACGGAGACATTTTGTCAGTTTTGCAACATTGGACCA
AATACAATGAAGTATTCTTGCTGTGCTCTGGTTTTGGCTGTCCTGGGCACAGAATTGCTGGGA
AGCCTCTGTTCGACTGTCAGATCCCCGAGGTTCAGAGGACGGATACAGCAGGAACGAAAAAA
CATCCGACCCAACATTATTCTTGTGCTTACCGATGATCAAGATGTGGAGCTGGGGTCCCTGC
AAGTCATGAACAAAACGAGAAAGATTATGGAACATGGGGGGGCCACCTTCATCAATGCC
TTTGTGACTACACCCATGTGCTGCCCGTCACGGTCCTCCATGCTCACCGGGAAGTATGT
GCACAATCACAATGTCTACACCAACAACGAGAACTGCTCTTCCCCCTCGTGGCAGGCCA
TGCATGAGCCTCGGACTTTTGCTGTATATCTTAACAACACTGGCTACAGAACAGCCTTTT
TTGGAAAATACCTCAATGAATATAATGGCAGCTACATCCCCCCTGGGTGGCGAGAATGG
CTTGGATTAATCAAGAATTCTCGCTTCTATAATTACACTGTTTGTCGCAATGGCATCAAA
GAAAAGCATGGATTTGATTATGCAAAGGACTACTTCACAGACTTAATCACTAACGAGAG
CATTAATTACTTCAAAATGTCTAAGAGAATGTATCCCCATAGGCCCGTTATGATGGTGAT
CAGCCACGCTGCGCCCCACGGCCCCGAGGACTCAGCCCCACAGTTTTCTAAACTGTACC
CCAATGCTTCCCAACACATAACTCCTAGTTATAACTATGCACCAAATATGGATAAACACT
GGATTATGCAGTACACAGGACCAATGCTGCCCATCCACATGGAATTTACAAACATTCTAC
AGCGCAAAAGGCTCCAGACTTTGATGTCAGTGGATGATTCTGTGGAGAGGCTGTATAAC
ATGCTCGTGGAGACGGGGGAGCTGGAGAATACTTACATCATTTACACCGCCGACCATGG
TTACCATATTGGGCAGTTTGGACTGGTCAAGGGGAAATCCATGCCATATGACTTTGATAT
TCGTGTGCCTTTTTTTATTCGTGGTCCAAGTGTAGAACCAGGATCAATAGTCCCACAGAT
CGTTCTCAACATTGACTTGGCCCCCACGATCCTGGATATTGCTGGGCTCGACACACCTCC
TGATGTGGACGGCAAGTCTGTCCTCAAACTTCTGGACCCAGAAAAGCCAGGTAACAGGT
TTCGAACAAACAAGAAGGCCAAAATTTGGCGTGATACATTCCTAGTGGAAAGAGGCAAA
TTTCTACGTAAGAAGGAAGAATCCAGCAAGAATATCCAACAGTCAAATCACTTGCCCAAA
TATGAACGGGTCAAAGAACTATGCCAGCAGGCCAGGTACCAGACAGCCTGTGAACAACC
GGGGCAGAAGTGGCAATGCATTGAGGATACATCTGGCAAGCTTCGAATTCACAAGTGTA
AAGGACCCAGTGACCTGCTCACAGTCCGGCAGAGCACGCGGAACCTCTACGCTCGCGGC
TTCCATGACAAAGACAAAGAGTGCAGTTGTAGGGAGTCTGGTTACCGTGCCAGCAGAAG
CCAAAGAAAGAGTCAACGGCAATTCTTGAGAAACCAGGGGACTCCAAAGTACAAGCCCA
GATTTGTCCATACTCGGCAGACACGTTCCTTGTCCGTCGAATTTGAAGGTGAAATATATG
ACATAAATCTGGAAGAAGAAGAAGAATTGCAAGTGTTGCAACCAAGAAACATTGCTAAG
CGTCATGATGAAGGCCACAAGGGGCCAAGAGATCTCCAGGCTTCCAGTGGTGGCAACAG
GGGCAGGATGCTGGCAGATAGCAGCAACGCCGTGGGCCCACCTACCACTGTCCGAGTG
ACACACAAGTGTTTTATTCTTCCCAATGACTCTATCCATTGTGAGAGAGAACTGTACCAA
TCGGCCAGAGCGTGGAAGGACCATAAGGCATACATTGACAAAGAGATTGAAGCTCTGCA
AGATAAAATTAAGAATTTAAGAGAAGTGAGAGGACATCTGAAGAGAAGGAAGCCTGAGG
AATGTAGCTGCAGTAAACAAAGCTATTACAATAAAGAGAAAGGTGTAAAAAAGCAAGAG
AAATTAAAGAGCCATCTTCACCCATTCAAGGAGGCTGCTCAGGAAGTAGATAGCAAACT
GCAACTTTTCAAGGAGAACAACCGTAGGAGGAAGAAGGAGAGGAAGGAGAAGAGACGG
CAGAGGAAGGGGGAAGAGTGCAGCCTGCCTGGCCTCACTTGCTTCACGCATGACAACAA
CCACTGGCAGACAGCCCCGTTCTGGAACCTGGGATCTTTCTGTGCTTGCACGAGTTCTA
ACAATAACACCTACTGGTGTTTGCGTACAGTTAATGAGACGCATAATTTTCTTTTCTGTG
AGTTTGCTACTGGCTTTTTGGAGTATTTTGATATGAATACAGATCCTTATCAGCTCACAA
ATACAGTGCACACGGTAGAACGAGGCATTTTGAATCAGCTACACGTACAACTAATGGAG
CTCAGAAGCTGTCAAGGATATAAGCAGTGCAACCCAAGACCTAAGAATCTTGATGTTGG
AAATAAAGATGGAGGAAGCTATGACCTACACAGAGGACAGTTATGGGATGGATGGGAAG
GTTGAATCAGCCCCGTCTCACTGCAGACATCAACTGGCAAGGCCTAGAGGAGCTACACAG
TGTGAATGAAAACATCTATGAGTACAGACAAAACTACAGACTTAGTCTGGTGGACTGGA

CTAATTACTTGAAGGATTTAGATAGAGTATTTGCACTGCTGAAGAGTCACTATGAGCAAA
ATAAAACAAATAAGACTCAAACTGCTCAAAGTGACGGGTTCTTGGTTGTCTCTGCTGAGC
ACGCTGTGTCAATGGAGATGGCCTCTGCTGACTCAGATGAAGACCCAAGGCATAAGGTT
GGGAAAACACCTCATTTGACCTTGCCAGCTGACCTTCAAACCCTGCATTTGAACCGACCA
ACATTAAGTCCAGAGAGTAAACTTGAATGGAATAACGACATTCCAGAAGTTAATCATTTG
AATTCTGAACACTGGAGAAAAACCGAAAAATGGACGGGGCATGAAGAGACTAATCATCT
GGAAACCGATTTCAGTGGCGATGGCATGACAGAGCTAGAGCTCGGGCCCAGCCCCAGG
CTGCAGCCCATTCGCAGGCACCCGAAAGAACTTCCCCAGTATGGTGGTCCTGGAAAGGA
CATTTTTGAAGATCAACTATATCTTCCTGTGCATTCCGATGGAATTTCAGTTCATCAGAT
GTTCACCATGGCCACCGCAGAACACCGAAGTAATTCCAGCATAGCGGGGAAGATGTTGA
CCAAGGTGGAGAAGAATCACGAAAAGGAGAAGTCACAGCACCTAGAAGGCAGCGCCTC
CTCTTCACTCTCCTCTGATTAGATGAAACTGTTACCTTACCCTAAACACAGTATTTCTTTT
TAACTTTTTTATTTGTAAACTAATAAAGGTAATCACAGCCACCAACATTCCAAGCTACCC
TGGGTACCTTTGTGCAGTAGAAGCTAGTGAGCATGTGAGCAAGCGGTGTGCACACGGAG
ACTCATCGTTATAATTTACTATCTGCCAAGAGTAGAAAGAAAGGCTGGGGATATTTGGGT
TGGCTTGGTTTTGATTTTTTGCTTGTTTGTTTGTTTTGTACTAAAACAGTATTATCTTTTG
AATATCGTAGGGACATAAGTATATACATGTTATCCAATCAAGATGGCTAGAATGGTGCCT
TTCTGAGTGTCTAAAACTTGACACCCCTGGTAAATCTTTCAACACACTTCCACTGCCTGC
GTAATGAAGTTTTGATTCATTTTTAACCACTGGAATTTTTCAATGCCGTCATTTTCAGTTA
GATGATTTTGCACTTTGAGATTAAAATGCCATGTCTATTTGATTAGTCTTATTTTTTTATT
TTTACAGGCTTATCAGTCTCACTGTTGGCTGTCATTGTGACAAAGTCAAATAAACCCCCA
AGGACGACACACAGTATGGATCACATATTGTTTGACATTAAGCTTTTGCCAGAAAATGTT
GCATGTGTTTTACCTCGACTTGCTAAAATCGATTAGCAGAAAGGCATGGCTAATAATGTT
GGTGGTGAAAATAAATAAATAAGTAAACAAAAWRAARAWWGCCTGCTCTCTCTGTGCC
TAGCCTCAAAGCGTTCATCATACATCATACCTTTAAGATTGCTATATTTTGGGTTATTTTC
TTGACAGGAGAAAAAGATCTAAAGATCTTTTATTTTCATCTTTTTTGGTTTTCTTGGCATG
ACTAAGAAGCTTAAATGTTGATAAAATATGACTAGTTTTGAATTTACACCAAGAACTTCT
CAATAAAAGAAAATCATGAATGCTCCACAATTTCAACATACCACAAGAGAAGTTAATTTC
TTAACATTGTGTTCTATGATTATTTGTAAGACCTTCACCAAGTTCTGATATCTTTTAAAGA
CATAGTTCAAAATTGCTTTTGAAAATCTGTATTCTTGAAAATATCCTTGTTGTGTATTAGG
TTTTTAAATACCAGCTAAAGGATTACCTCACTGAGTCATCAGTACCCTCCTATTCAGCTC
CCCAAGATGATGTGTTTTTGCTTACCCTAAGAGAGGTTTTCTTCTTATTTTTAGATAATTC
AAGTGCTTAGATAAATTATGTTTTCTTTAAGTGTTTATGGTAAACTCTTTTAAAGAAAATT
TAATATGTTATAGCTGAATCTTTTTGGTAACTTTAAATCTTTATCATAGACTCTGTACATA
TGTTCAAATTAGCTGCTTGCCTGATGTGTGTATCATCGGTGGGATGACAGAACAAACATA
TTTATGATCATGAATAATGTGCTTTGTAAAAAGATTTCAAGTTATTAGGAAGCATACTCT
GTTTTTTAATCATGTATAATATTCCATGATACTTTTATAGAACAATTCTGGCTTCAGGAAA
GTCTAGAAGCAATATTTCTTCAAATAAAAGGTGTTTAAACTTTAAAAAAAAAAAAAAAAA
AAAAAAAAAAA

FIGURE 49B

FIGURE 50

MKYSGCALVLAVLGLLLLGSLGSTVRSPRFRGRIQQERKNIRPNIILVLTDDQDVELGSLQVMNKT
RKIMEHGGATFINAFVTTPMCCPSRSSMLTGKYVHNHNVYTNNENCSSPSWQAMHEPRTFAVYL
NNTGYRTAFFGKYLNEYNGSYIPPGWREWLGLIKNSRFYNYTVCRNGIKEKHGFDYAKDYFTDLI
TNESINYFKMSKRMYPHRPVMMVISHAAPHGPEDSAPQFSKLYPNASQHITPSYNYAPNMDKHWI
MQYTGPMLPIHMEFTNILQRKRLQTLMSVDDSVERLYNMLVETGELENTYIIYTADHGYHIGQFG
LVKGKSMPYDFDIRVPFFIRGPSVEPGSIVPQIVLNIDLAPTILDIAGLDTPPDVDGKSVLKLLDPEKP
GNRFRTNKKAKIWRDTFLVERGKFLRKKEESSKNIQQSNHLPKYERVKELCQQARYQTACEQPGQ
KWQCIEDTSGKLRIHKCKGPSDLLTVRQSTRNLYARGFHDKDKECSCRESGYRASRSQRKSQRQF
LRNQGTPKYKPRFVHTRQTRSLSVEFEGEIYDINLEEEEELQVLQPRNIAKRHDEGHKGPRDLQASS
GGNRGRMLADSSNAVGPPTTVRVTHKCFILPNDSIHCERELYQSARAWKDHKAYIDKEIEALQDKI
KNLREVRGHLKRRKPEECSCSKQSYYNKEKGVKKQEKLKSHLHPFKEAAQEVDSKLQLFKENNR
RRKKERKEKRRQRKGEECSLPGLTCFTHDNNHWQTAPFWNLGSFCACTSSNNNTYWCLRTVNET
HNFLFCEFATGFLEYFDMNTDPYQLTNTVHTVERGILNQLHVQLMELRSCQGYKQCNPRPKNLDV
GNKDGGSYDLHRGQLWDGWEG

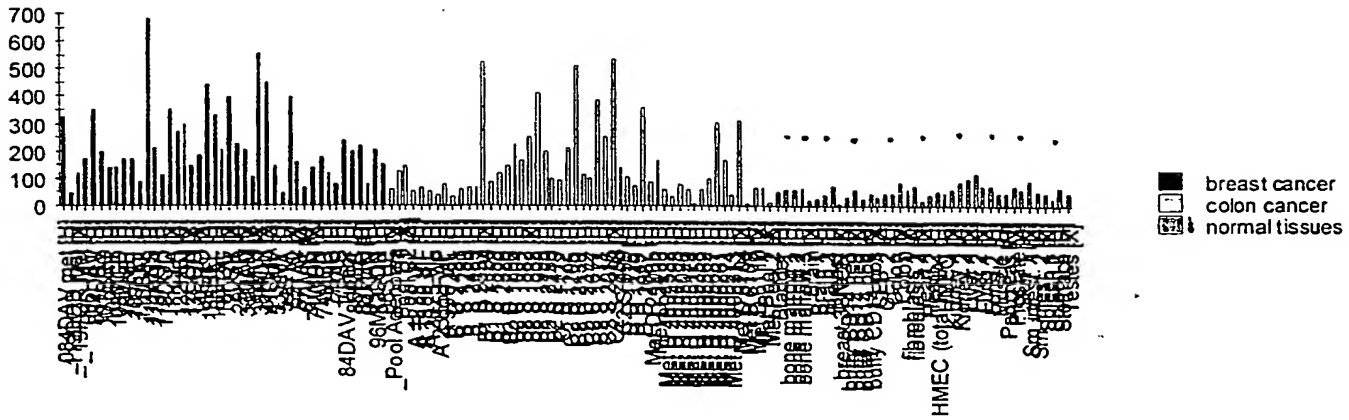


FIGURE 51

AACCGAGAAGCGCTCCGTAAAGCCATCCGCACGCTCAGAAAGGCCGTCCACAGGGAGCAGTTTCACCTCCAGCTCTCAGG
CATGAACCTCGACGTGGCTAAAAAGCCTCCCAGAACATCTGAACGCCAGGCAGAGTCCTGTGGAGTGGGCCAGGGTCATG
CAGAAAACCAATGTGTCAGTTGCAGGGCTGGGACCTATTATGATGGAGCACGAGAACGCTGCATTTTATGTCCAAATGGA
ACCTTCCAAAATGAGGAAGGACAAATGACTTGTGAACCATGCCCAAGACCAGGAAATTCTGGGGCCCTGAAGACCCCAGA
AGCTTGGAATATGTCTGAATGTGGAGGKCTGTGTCAACCTACTGAATATTCTGCAGATGGCTTTGCACCTTGCCAGCTCT
GTGCCCTGGGCASGTTCCAGCCTGAAGCTGGTCGAACTTCCTGCTTCCCCTGTGGAGGAGGCCTTGCCACCAAACATCAG
GGAGCTACTTCCTTTCAGGACTGTGAAACCAGAGTTCAATGTTCACCTGGACATTTCTACAACACCACCACTCACCGATG
TATTCGTTGCCCAGTGGGAACATACCAGCCTGAATTTGGAAAAAATAATTGTGTTTCTTGCCCAGGAAATACTACGACTG
ACTTTGATGGCTCCACAAACATAACCCAGTGTAAAAACAGAAGATGTGGAGGGGAGCTGGGAGATTTCACTGGGTACATT
GAATCCCCAAACTACCCAGGCAATTACCCAGCCAACACCGAGTGTACGTGGACCATCAACCCACCCCCCAAGCGCCGCAT
CCTGATCGTGGTCCCTGAGATCTTCCTGCCCATAGAGGACGACTGTGGGGACTATCTGGTGATGCGGAAAACCTCTTCAT
CCAATTCTGTGACAACATATGAAACCTGCCAGACCTACGAACGCCCCATCGCCTTCACCTCCAGGTCAAAGAAGCTGTGG
ATTCAGTTCAAGTCCAATGAAGGGAACAGCGCTAGAGGGTTCCAGGTCCCATACGTGACATATGATGAGGACTACCAGGA
ACTCATTGAAGACATAGTTCGAGATGGCAGGCTCTATGCATCTGAGAACCATCAGGAAATACTTAAGGATAAGAAACTTA
TCAAGGCTCTGTTTGATGTCCTGGCCCATCCCCAGAACTATTTCAAGTACACAGCCCAGGAGTCCCGAGAGATGTTTCCA
AGATCGTTCATCCGATTGCTACGTTCCAAAGTGTCCAGGTTTTTGAGACCTTACAAATGACTCAGCCCACGTGCCACTCA
ATACAAATGTTCTGCTATAGGGTTGGTGGGACAGAGCTGTCTTCCTTCTGCATGTCAGCACAGTCGGGTATTGCTGCCTC
CCGTATCAGTGACTCATTAGAGTTCAATTTTTATAGATAATACAGATATTTTGGTAAATTGAACTTGGTTTTTCTTTCCC
AGCATCGTGGATGTAGACTGAGAATGGCTTTGAGTGGCATCAGCTTCTCACTGCTGTGGGCGGATGTCTTGGATAGATCA
AGGGCTGGCTGAGCTGGACTTTGGTCAGCCTAGGTGAGACTCACCTGTCCTTCTGGGGTCTTACTCCTCCTCAAGGAGTC
TGTAGTGGAAAGGAGGCCACAGAATAAGCTGCTTATTCTGAAACTTCAGCTTCCTCTAGCCCGGCCCTCTCTAAGGGAGC
CCTCTGCACTCGTGTGCAGGCTCTGACCAGGCAGAACAGGCAAGAGGGGAGGGAAGGAGACCCCTGCAGGCTCCCTCCAC
CCACCTTGAGACCTGGGAGGACTCAGTTTCTCCACAGCCTTCTCCAGCCTGTGTGATACAAGTTTGATCCCAGGAACTTG
AGTTCTAAGCAGTGCTCGTGAAAAAAAAAAAGCAGAAAGAATTAGAAATAAATAAAAACTAAGCACTTCTGGAGACATAAA
AA

FIGURE 5 2

FIGURE 53

...ATGAACCTCGACGTGGCTAAAAAGCCTCCCAGAACATCTGAACGCCAGGCAGAGTCCTGTGGAGTGGGCCAGGGTCA
TGCAGAAAACCAATGTGTCAGTTGCAGGGCTGGGACCTATTATGATGGAGCACGAGAACGCTGCATTTTATGTCCAAATG
GAACCTTCCAAAATGAGGAAGGACAAATGACTTGTGAACCATGCCCAAGACCAGGAAATTCTGGGGCCCTGAAGACCCCA
GAAGCTTGGAATATGTCTGAATGTGGAGGKCTGTGTCAACCTACTGAATATTCTGCAGATGGCTTTGCACCTTGCCAGCT
CTGTGCCCTGGGCASGTTCCAGCCTGAAGCTGGTCGAACTTCCTGCTTCCCCTGTGGAGGAGGCCTTGCCACCAAACATC
AGGGAGCTACTTCCTTTCAGGACTGTGAAACCAGAGTTCAATGTTCACCTGGACATTTCTACAACACCACCACTCACCGA
TGTATTCGTTGCCCAGTGGGAACATACCAGCCTGAATTTGGAAAAAATAATTGTGTTTCTTGCCCAGGAAATACTACGAC
TGACTTTGATGGCTCCACAAACATAACCCAGTGTAAAAACAGAAGATGTGGAGGGGAGCTGGGAGATTTCACTGGGTACA
TTGAATCCCCAAACTACCCAGGCAATTACCCAGCCAACACCGAGTGTACGTGGACCATCAACCCACCCCCCAAGCGCCGC
ATCCTGATCGTGGTCCCTGAGATCTTCCTGCCCATAGAGGACGACTGTGGGGACTATCTGGTGATGCGGAAAACCTCTTC
ATCCAATTCTGTGACAACATATGAAACCTGCCAGACCTACGAACGCCCCATCGCCTTCACCTCCAGGTCAAAGAAGCTGT
GGATTCAGTTCAAGTCCAATGAAGGGAACAGCGCTAGAGGGTTCCAGGTCCCATACGTGACATATGATGAGGACTACCAG
GAACTCATTGAAGACATAGTTCGAGATGGCAGGCTCTATGCATCTGAGAACCATCAGGAAATACTTAAGGATAAGAAACT
TATCAAGGCTCTGTTTGATGTCCTGGCCCATCCCCAGAACTATTTCAAGTACACAGCCCAGGAGTCCCGAGAGATGTTTC
CAAGATCGTTCATCCGATTGCTACGTTCCAAAGTGTCCAGGTTTTTGAGACCTTACAAATGA

FIGURE 54

...MNLDVAKKPPRTSERQAESCGVGQGHAENQCVSCRAGTYYDGARERCILCPNGTFQNEEGQMTCEPCPRPGNSGALK
TPEAWNMSECGGLCQPTEYSADGFAPCQLCALGXFQPEAGRTSCFPCGGGLATKHQGATSFQDCETRVQCSPGHFYNTTT
HRCIRCPVGTYQPEFGKNNCVSCPGNTTTDFDGSTNITQCKNRRCGGELGDFTGYIESPNYPGNYPANTECTWTINPPPK
RRILIVVPEIFLPIEDDCGDYLVMRKTSSSNSVTTYETCQTYERPIAFTSRSKKLWIQFKSNEGNSARGFQVPYVTYDED
YQELIEDIVRDGRLYASENHQEILKDKKLIKALFDVLAHPQNYFKYTAQESREMFPRSFIRLLRSKVSRFLRPYK.

```
human_BCO2      MNLDVAKKPPRTSERQAESCGVGQGHAENQCVSCRAGTYYDGARERCILCPNGTFQNEEG
mouse_BCO2      ------------------------------------------------------------

human_BCO2      QMTCEPCPRPGNSGALKTPEAWNMSECGGLCQPTEYSADGFAPCQLCALGXFQPEAGRTS
mouse_BCO2      ------------------------------------------------------------

human_BCO2      CFPCGGGLATKHQGATSFQDCETRVQCSPGHFYNTTTHRCIRCPVGTYQPEFGKNNCVSC
mouse_BCO2      ------------------------------------------------------------

human_BCO2      PGNTTTDFDGSTNITQCKNRRCGGELGDFTGYIESPNYPGNYPANTECTWTINPPPKRRI
mouse_BCO2      -----------------------------------------------------TINPPPKRRI
                                                                    **********

human_BCO2      LIVVPEIFLPIEDDCGDYLVMRKTSSSNSVTTYETCQTYERPIAFTSRSKKLWIQFKSNE
mouse_BCO2      LIVVPEIFLPIEDDCGDYLVMRKTSSSNSVTTYETCQTYERPIAFTSRSKKLWIQFKSNE
                ************************************************************

human_BCO2      GNSARGFQVPYVTYDEDYQELIEDIVRDGRLYASENHQEILKDKKLIKALFDVLAHPQNY
mouse_BCO2      GNSARGFQVPYVTYDEDYQELIEDIVRDGRLYASENHQEILKDKKLIKALFDVLAHPQNY
                ************************************************************

human_BCO2      FKYTAQESREMFPRSFIRLLRSKVSRFLRPYK
mouse_BCO2      FKYTAQESREMFPRSFIRLLRSKVSRFLRPYK
                ********************************
```

FIGURE 55

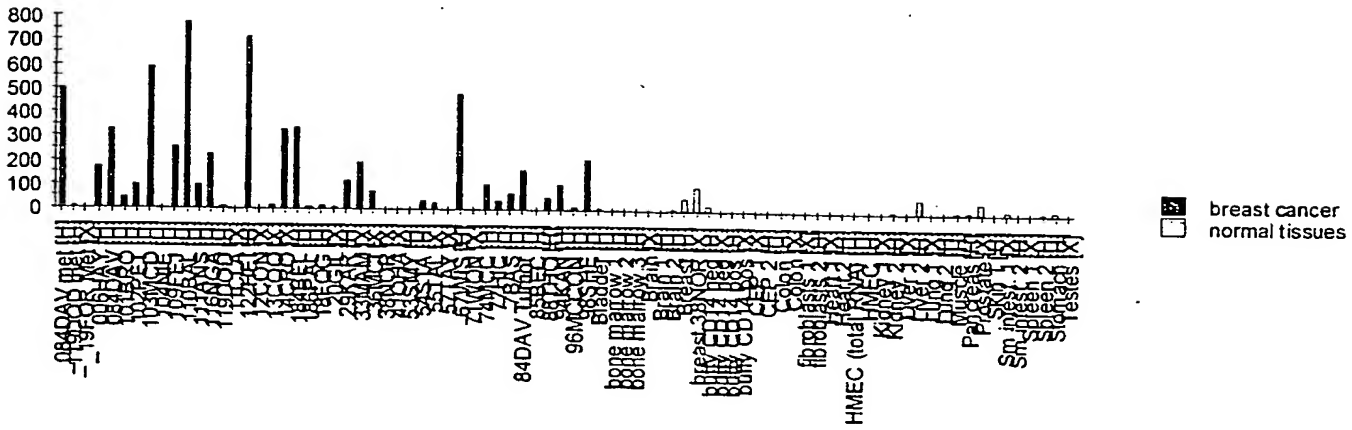


FIGURE 56

CAGCGGCCGCTGAATTCTAGGGCGGGTTCGCGCCCCGAAGGCTGAGAGCTGGCGCTGCTCGTGCCCTGTG
TGCCAGACGGCGGAGCTCCGCGGCCGGACCCCGCGGCCCCGCTTTGCTGCCGACTGGAGTTTGGGGGAAG
AAACTCTCCTGCGCCCCAGAAGATTTCTTCCTCGGCGAAGGGACAGCGAAAGATGAGGGTGGCAGGAAGA
GAAGGCGCTTTCTGTCTGCCGGGGTCGCAGCGCGAGAGGGCAGTGCCATGTTCCTCTCCATCCTAGTGGC
GCTGTGCCTGTGGCTGCACCTGGCGCTGGGCGTGCGCGGCGCGCCCTGCGAGGCGGTGCGCATCCCTATG
TGCCGGCACATGCCCTGGAACATCACGCGGATGCCCAACCACCTGCACCACAGCACGCAGGAGAACGCCA
TCCTGGCCATCGAGCAGTACGAGGAGCTGGTGGACGTGAACTGCAGCGCCGTGCTGCGCTTCTTCTTCTG
TGCCATGTACGCGCCCATTTGCACCCTGGAGTTCCTGCACGACCCTATCAAGCCGTGCAAGTCGGTGTGC
CAACGCGCGCGCGACGACTGCGAGCCCCTCATGAAGATGTACAACCACAGCTGGCCCGAAAGCCTGGCCT
GCGACGAGCTGCCTGTCTATGACCGTGGCGTGTGCATTTCGCCTGAAGCCATCGTCACGGACCTCCCGGA
GGATGTTAAGTGGATAGACATCACACCAGACATGATGGTACAGGAAAGGCCTCTTGATGTTGACTGTAAA
CGCCTAAGCCCCGATCGGTGCAAGTGTAAAAAGGTGAAGCCAACTTTGGCAACGTATCTCAGCAAAAACT
ACAGCTATGTTATTCATGCCAAAATAAAAGCTGTGCAGAGGAGTGGCTGCAATGAGGTCACAACGGTGGT
GGATGTAAAAGAGATCTTCAAGTCCTCATCACCCATCCCTCGAACTCAAGTCCCGCTCATTACAAATTCT
TCTTGCCAGTGTCCACACATCCTGCCCCATCAAGATGTTCTCATCATGTGTTACGAGTGGCGTTCAAGGA
TGATGCTTCTTGAAAATTGCTTAGTTGAAAAATGGAGAGATCAGCTTAGTAAAAGATCCATACAGTGGGA
AGAGAGGCTGCAGGAACAGCGGAGAACAGTTCAGGACAAGAAGAAAACAGCCGGGCGCACCAGTCGTAGT
AATCCCCCCAAACCAAAGGGAAAGCCTCCTGCTCCCAAACCAGCCAGTCCCAAGAAGAACATTAAAACTA
GGAGTGCCCAGAAGAGAACAAACCCGAAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAGACTTCCGAC
TTCCTTACAGGATGAGGCTGGGCATTGCCTGGGACAGCCTATGTAAGGCCATGTGCCCCTTGCCCTAACA
ACTCACTGCAGTGCTCTTCATAGACACATCTTGCAGCATTTTTCTTAAGGCTATGCTTCAGTTTTTCTTT
GTAAGCCATCACAAGCCATAGTGGTAGGTTTGCCCTTTGGTACAGAAGGTGAGTTAAAGCTGGTGGAAAA
GGCTTATTGCATTGCATTCAGAGTAACCTGTGTGCATACTCTAGAAGAGTAGGGAAAATAATGCTTGTTA
CAATTCGACCTAATATGTGCATTGTAAAATAAATGCCATATTTCAAACAAAACACGTAATTTTTTTACAG
TATGTTTTATTACCTTTTGATATCTGTTGTTGCAATGTTAGTGATGTTTTAAAATGTGATGAAAATATAA
TGTTTTTAAGAAGGAACAGTAGTGGAATGAATGTTAAAAGATCTTTATGTGTTTATGGTCTGCAGAAGGA
TTTTTGTGATGAAAGGGGATTTTTTGAAAAATTAGAGAAGTAGCATATGGAAAATTATAATGTGTTTTTT
TACCAATGACTTCAGTTTCTGTTTTTAGCTAGAAACTTAAAAACAAAAATAATAATAAAGAAAAATAAAT
AAAAAGGAGAGGCAGACAATGTCTGGATTCCTGTTTTTTGGTTACCTGATTTCCATGATCATGATGCTTC
TTGTCAACACCCTCTTAAGCAGCACCAGAAACAGTGAGTTTGTCTGTACCATTAGGAGTTAGGTACTAAT
TAGTTGGCTAATGCTCAAGTATTTTATACCCACAAGAGAGGTATGTCACTCATCTTACTTCCCAGGACAT
CCACCCTGAGAATAATTTGACAAGCTTAAAAATGGCCTTCATGTGAGTGCCAAATTTTGTTTTTCTTCAT
TTAAATATTTTCTTTGCCTAAATACATGTGAGAGGAGTTAAATATAAATGTACAGAGAGGAAAGTTGAGT
TCCACCTCTGAAATGAGAATTACTTGACAGTTGGGATACTTTAATCAGAAAAAAAGAACTTATTTGCAGC
ATTTTATCAACAAATTTCATAATTGTGGACAATTGGAGGCATTTATTTTAAAAAACAATTTTATTGGCCT
TTTGCTAACACAGTAAGCATGTATTTTATAAGGCATTCAATAAATGCACAACGCCCAAAGGAAATAAAAT
CCTATCTAATCCTACTCTCCACTACACAGAGGTAATCACTATTAGTATTTTGGCATATTATTCTCCAGGT
GTTTGCTTATGCACTTATAAAATGATTTGAACAAATAAAACTAGGAACCTGTATACATGTGTTTCATAAC
CTGCCTCCTTTGCTTGGCCCTTTATTGAGATAAGTTTTCCTGTCAAGAAAGCAGAAACCATCTCATTTCT
AACAGCTGTGTTATATTCCATAGTATGCATTACTCAACAAACTGTTGTGCTATTGGATACTTAGGTGGTT
TCTTCACTGACAATACTGAATAAACATCTCACCGGAATTC

FIGURE 57

ATGTTCCTCTCCATCCTAGTGGC
GCTGTGCCTGTGGCTGCACCTGGCGCTGGGCGTGCGCGGCGCGCCCTGCGAGGCGGTGCGCATCCCTATG
TGCCGGCACATGCCCTGGAACATCACGCGGATGCCCAACCACCTGCACCACAGCACGCAGGAGAACGCCA
TCCTGGCCATCGAGCAGTACGAGGAGCTGGTGGACGTGAACTGCAGCGCCGTGCTGCGCTTCTTCTTCTG
TGCCATGTACGCGCCCATTTGCACCCTGGAGTTCCTGCACGACCCTATCAAGCCGTGCAAGTCGGTGTGC
CAACGCGCGCGCGACGACTGCGAGCCCCTCATGAAGATGTACAACCACAGCTGGCCCGAAAGCCTGGCCT
GCGACGAGCTGCCTGTCTATGACCGTGGCGTGTGCATTTCGCCTGAAGCCATCGTCACGGACCTCCCGGA
GGATGTTAAGTGGATAGACATCACACCAGACATGATGGTACAGGAAAGGCCTCTTGATGTTGACTGTAAA
CGCCTAAGCCCCGATCGGTGCAAGTGTAAAAAGGTGAAGCCAACTTTGGCAACGTATCTCAGCAAAAACT
ACAGCTATGTTATTCATGCCAAAATAAAAGCTGTGCAGAGGAGTGGCTGCAATGAGGTCACAACGGTGGT
GGATGTAAAAGAGATCTTCAAGTCCTCATCACCCATCCCTCGAACTCAAGTCCCGCTCATTACAAATTCT
TCTTGCCAGTGTCCACACATCCTGCCCCATCAAGATGTTCTCATCATGTGTTACGAGTGGCGTTCAAGGA
TGATGCTTCTTGAAAATTGCTTAGTTGAAAAATGGAGAGATCAGCTTAGTAAAAGATCCATACAGTGGGA
AGAGAGGCTGCAGGAACAGCGGAGAACAGTTCAGGACAAGAAGAAAACAGCCGGGCGCACCAGTCGTAGT
AATCCCCCCAAACCAAAGGGAAAGCCTCCTGCTCCCAAACCAGCCAGTCCCAAGAAGAACATTAAAACTA
GGAGTGCCCAGAAGAGAACAAACCCGAAAAGAGTGTGA

FIGURE 58

MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYEELVDVNCS
AVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPESLACDELPVYDRGVCISPE
AIVTDLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRCKCKKVKPTLATYLSKNYSYVIHAKIKAVQRSG
CNEVTTVVDVKEIFKSSSPIPRTQVPLITNSSCQCPHILPHQDVLIMCYEWRSRMMLLENCLVEKWRDQL
SKRSIQWEERLQEQRRTVQDKKKTAGRTSRSNPPKPKGKPPAPKPASPKKNIKTRSAQKRTNPKRV

FIGURE 59

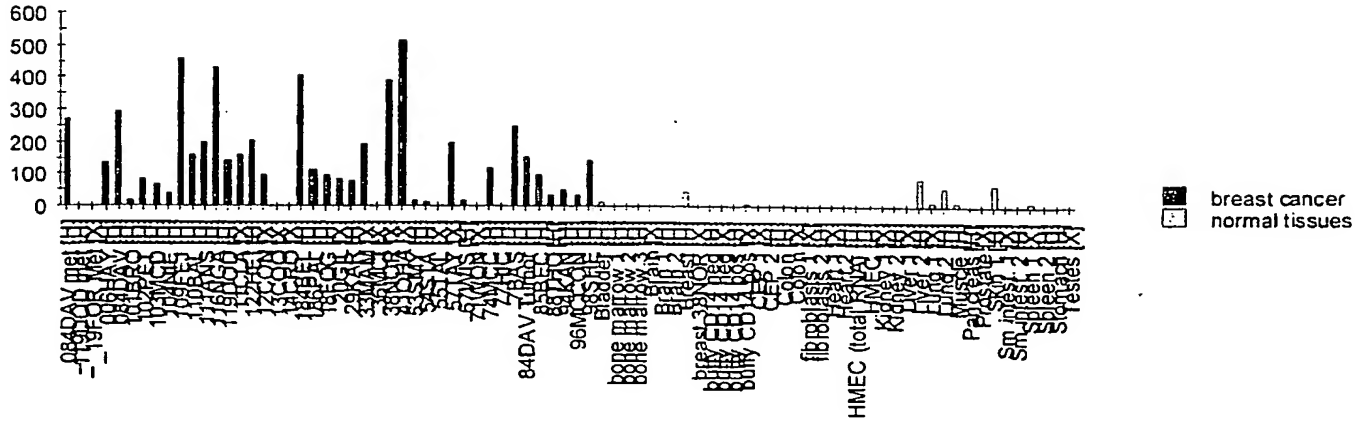


FIGURE 60

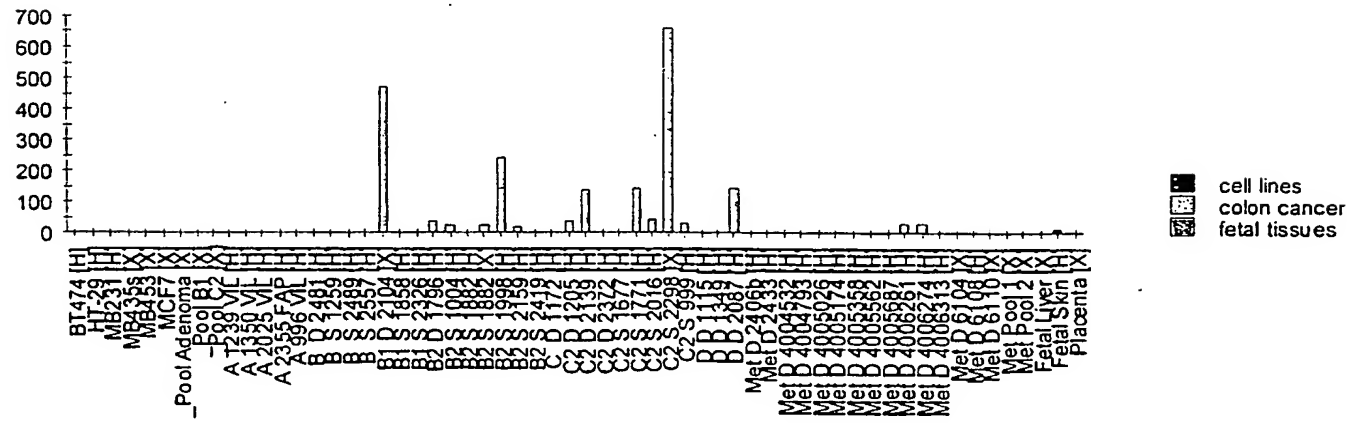


FIGURE6 1

CGGCACCAAGAGCACTGGCCAAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGACATGATGCTACACTCAGCTTTGGGTCT
CTGCCTCTTACTCGTCACAGTTTCTTCCAACCTTGCCATTGCAATAAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAA
GAGGATGGGGAGATGACATCACTTGGGTACAAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAAGTAAGAAGCCATTA
ATGGTTATTCATCACCTGGAGGATTGTCAATACTCTCAAGCACTAAAGAAAGTATTTGCCCAAAATGAAGAAATACAAGA
AATGGCTCAGAATAAGTTCATCATGCTAAACCTTATGCATGAAACCACTGATAAGAATTTATCACCTGATGGGCAATATG
TGCCTAGAATCATGTTTGTAGACCCTTCTTTAACAGTTAGAGCTGACATAGCTGGAAGATACTCTAACAGATTGTACACA
TATGAGCCTCGGGATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAGACTTATTCAGTCAGAGCTATAAGAGAT
GATAGAAAAAAGCCTTCACTTCAAAGAAGTCAAATTTCATGAAGAAAACCTCTGGCACATTGACAAATACTAAATGTGCA
AGTATATAGATTTTGTAATATTACTATTTAGTTTTTTTAATGTGTTTGCAATAGTCTTATTAAAATAAATGTTTTTTAAA
TCTGAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 62

ATGATGCTACACTCAGCTTTGGGTCTCTGCCTCTTACTCGTCACAGTTTCTTCCAACCTTGCCATTGCAATAAAAAAGGA
AAAGAGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGACATCACTTGGGTACAAACTTATGAAGAAGGTCTCTTTT
ATGCTCAAAAAAGTAAGAAGCCATTAATGGTTATTCATCACCTGGAGGATTGTCAATACTCTCAAGCACTAAAGAAAGTA
TTTGCCCAAAATGAAGAAATACAAGAAATGGCTCAGAATAAGTTCATCATGCTAAACCTTATGCATGAAACCACTGATAA
GAATTTATCACCTGATGGGCAATATGTGCCTAGAATCATGTTTGTAGACCCTTCTTTAACAGTTAGAGCTGACATAGCTG
GAAGATACTCTAACAGATTGTACACATATGAGCCTCGGGATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAGA
CTTATTCAGTCAGAGCTATAA

FIGURE 63

MMLHSALGLCLLLVTVSSNLAIAIKKEKRPPQTLSRGWGDDITWVQTYEEGLFYAQKSKKPLMVIHHLEDCQYSQALKKV
FAQNEEIQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRIMFVDPSLTVRADIAGRYSNRLYTYEPRDLPLLIENMKKALR
LIQSEL

FIGURE 64

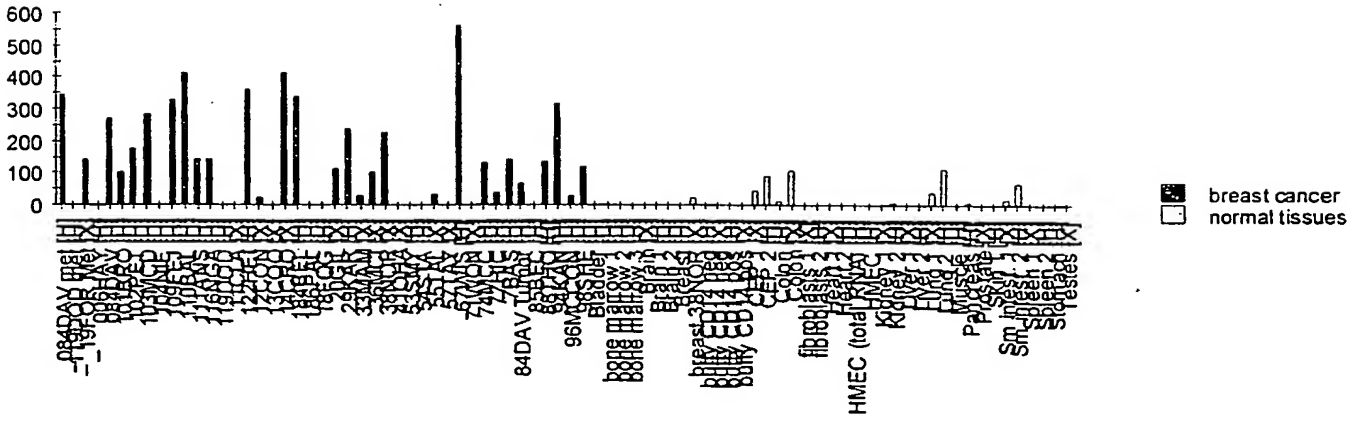


FIGURE 65

AGCGGCCGGGGCCACGGGGAGCGCGACGGCTGCGCGGGGGGCGGGAGCCGCGGCGGCGAG
GGCGGGCGCGCTCCCCGGGAGGGCCCGGCGGGGAACGGCCGCGATCGGGGCCGCAGCCACG
CTGCCGAGGCGCCCGGGGACCCGCAGGCGGCCGCGTCCTTGCTGGCCCCTATGGACGTGGGG
GAGGAGCCGCTGGAGAAGGCGGCGCGCGCCCGCACTGCCAAGGACCCCAACACCTATAAAGT
ACTCTCGCTGGTATTGTCAGTATGTGTGTTAACAACAATACTTGGTTGTATATTTGGGTTGAAA
CCAAGCTGTGCCAAAGAAGTTAAAAGTTGCAAAGGTCGCTGTTTCGAGAGAACATTTGGGAA
CTGTCGCTGTGATGCTGCCTGTGTTGAGCTTGGAAACTGCTGTTTAGATTACCAGGAGACGTG
CATAGAACCAGAACATATATGGACTTGCAACAAATTCAGGTGTGGTGAGAAAAGGTTGACCA
GAAGCCTCTGTGCCTGTTCAGATGACTGCAAGGACAAGGGCGACTGCTGCATCAACTACAGTT
CTGTGTGTCAAGGTGAGAAAAGTTGGGTAGAAGAACCATGTGAGAGCATTAATGAGCCACAG
TGCCCAGCAGGGTTTGAAACGCCTCCTACCCTCTTATTTTCTTTGGATGGATTCAGGGCAGAAT
ATTTACACACTTGGGGTGGACTTCTTCCTGTTATTAGCAAACTAAAAAAATGTGGAACATATA
CTAAAAACATGAGACCGGTATATCCAACAAAAACTTTCCCCAATCACTACAGCATTGTCACCG
GATTGTATCCAGAATCTCATGGCATAATCGACAATAAAATGTATGATCCCAAAATGAATGCTT
CCTTTTCACTTAAAAGTAAAGAGAAATTTAATCCTGAGTGGTACAAAGGAGAACCAATTTGGG
TCACAGCTAAGTATCAAGGCCTCAAGTCTGGCACATTTTTCTGGCCAGGATCAGATGTGGAAA
TTAACGGAATTTTCCCAGACATCTATAAAATGTATAATGGTTCAGTACCATTTGAAGAAAGGA
TTTTAGCTGTTCTTCAGTGGCTACAGCTTCCTAAAGATGAAAGACCACACTTTTACACTCTGTA
TTTAGAAGAACCAGATTCTTCAGGTCATTCATATGGACCAGTCAGCAGTGAAGTCATCAAAGC
CTTGCAGAGGGTTGATGGTATGGTTGGTATGCTGATGGATGGTCTGAAAGAGCTGAACTTGCA
CAGATGCCTGAACCTCATCCTTATTTCAGATCATGGCATGGAACAAGGCAGTTGTAAGAAATA
CATATATCTGAATAAATATTTGGGGGATGTTAAAAATATTAAAGTTATCTATGGACCTGCAGC
TCGATTGAGACCCTCTGATGTCCCAGATAAATACTATTCATTTAACTATGAAGGCATTGCCCG
AAATCTTTCTTGCCGGGAACCAAACCAGCACTTCAAACCTTACCTGAAACATTTCTTACCTAA
GCGTTTGCACTTTGCTAAGAGTGATAGAATTGAGCCCTTGACATTCTATTTGGACCCTCAGTGG
CAACTTGCATTGAATCCCTCAGAAAGGAAATATTGTGGAAGTGGATTTCATGGCTCTGACAAT
GTATTTTCAAATATGCAAGCCCTCTTTGTTGGCTATGGACCTGGATTCAAGCATGGCATTGAG
GCTGACACCTTTGAAAACATTGAAGTCTATAACTTAATGTGTGATTTACTGAATTTGACACCG
GCTCCTAATAACGGAACTCATGGAAGTCTTAACCACCTTCTAAAGAATCCTGTTTATACGCCA
AAGCATCCCAAAGAAGTGCACCCCCTGGTACAGTGCCCCTTCACAAGAAACCCCAGAGATAA
CCTTGGCTGCTCATGTAACCCTTCGATTTTGCCGATTGAGGATTTTCAAACACAGTTCAATCTG
ACTGTGGCAGAAGAGAAGATTATTAAGCATGAAACTTTACCCTATGGAAGACCTAGAGTTCTC
CAGAAGGAAAACACCATCTGTCTTCTTTCCCAGCACCAGTTTATGAGTGGATACAGCCAAGAC
ATCTTAATGCCCCTTTGGACATCCTATACCGTGGACAGAAATGACAGTTTCTCTACGGAAGAC
TTCTCCAACTGTCTGTACCAGGACTTTAGAATTCCTCTTAGTCCTGTCCATAAATGTTCATTTTA
TAAAAATAACACCAAAGTGAGTTACGGGTTCCTCTCCCCACCACAACTAAATAAAAATTCAAG
TGGAATATATTCTGAAGCTTTGCTTACTACAAATATAGTGCCAATGTACCAGAGTTTTCAAGTT
ATATGGCGCTACTTTCATGACACCCTACTGCGAAAGTATGCTGAAGAAAGAAATGGTGTCAAT
GTCGTCAGTGGTCCTGTGTTTGACTTTGATTATGATGGACGTTGTGATTCCTTAGAGAATCTGA
GGCAAAAAAAGAAGAGTCATCCGTAACCAAGAAATTTTGATTCCAACTCACTTCTTTATTGTGC
TAACAAGCTGTAAAGATACATCTCAGACGCCTTTGCACTGTGAAAACCTAGACACCTTAGCTT
TCATTTTGCCTCACAGGACTGATAACAGCGAGAGCTGTGTGCATGGGAAGCATGACTCCTCAT
GGGTTGAAGAATTGTTAATGTTACACAGAGCACGGATCACAGATGTTGAGCACATCACTGGA
CTCAGCTTCTATCAACAAAGAAAAGAGCCAGTTTCAGACATTTTAAAGTTGAAAACACATTTG
CCAACCTTTAGCCAAGAAGACTATGTTTTTTATCCCCAAACACCATGAATCTTTTTGAGA
GAACCTTATATTTTATATAGTCCTCTAGCTACACTATTGCATTGTTCAGAAACTGTCGA:CCAG
AGT:TAGAACGGAGCCCTCGGTGATGCGGACATCTCAGGGAAACTTGCGTACTCAGCACAGCA
GTGGAGAGTGTTCCTGTTGAATCTTGCACATATTTGAATGTGTAAGCATTGTATACATTGATCA
AGTTCGGGGGAATAAAGACAGACCACACCTAAAACTGCCTTTCTGCTTCTCTTAAAGGAGAAG
TAGCTGTGAACATTGTCTGGATACCAGATATTTGAATCTTTCTTACTATTGGTAATAAACCTTG
ATGGCATTGGGCAAACAGTAGACTTATAGTAGGGTTGGGGTAGCCCATGTTATGTGACTATCT
TTATGAGAATTTTAAAGTGGTTCTGGATATCTTTTAACTTGGAGTTTCATTTCTTTTCATTGTAA
TCAAAAAAAAAAATTAACAGAAGCCAAAATACTTCTGAGACCTTGTTTCAATCTTTGCTGTATA
TCCCCTCAAAATCCAAGTTATTAATCTTATGTGTTTTCTTTTTAATTTTTTGATTGGATTTCTTT
AGATTTAATGGTTCAAATGAGTTCAACTTTGAGGGACGATCTTTGAATATACTTACCTATTATA
AAATCTTACTTTGTATTTGTATTT

FIGURE 66

MERDGCAGGGSRGGEGGRAPREGPAGNGRDRGRSHAAEAPGDPQAAASLLAPMDVGEEPLEKA
ARARTAKDPNTYKVLSLVLSVCVLTTILGCIFGLKPSCAKEVKSCKGRCFERTFGNCRCDAACVEL
GNCCLDYQETCIEPEHIWTCNKFRCGEKRLTRSLCACSDDCKDKGDCCINYSSVCQGEKSWVEEP
CESINEPQCPAGFETPPTLLFSLDGFRAEYLHTWGGLLPVISKLKKCGTYTKNMRPVYPTKTFPNH
YSIVTGLYPESHGIIDNKMYDPKMNASFSLKSKEKFNPEWYKGEPIWVTAKYQGLKSGTFFWPGS
DVEINGIFPDIYKMYNGSVPFEERILAVLQWLQLPKDERPHFYTLYLEEPDSSGHSYGPVSSEVIKA
LQRVDGMVGMLMDGLKELNLHRCLNLILISDHGMEQGSCKKYTYLNKYLGDVKNIKVIYGPAAR
LRPSDVPDKYYSFNYEGIARNLSCREPNQHFKPYLKHFLPKRLHFAKSDRIEPLTFYLDPQWQLAL
NPSERKYCGSGFHGSDNVFSNMQALFVGYGPGFKHGIEADTFENIEVYNLMCDLLNLTPAPNNGT
HGSLNHLLKNPVYTPKHPKEVHPLVQCPFTRNPRDNLGCSCNPSILPIEDFQTQFNLTVAEEKIIKHE
TLPYGRPRVLQKENTICLLSQHQFMSGYSQDILMPLWTSYTVDRNDSFSTEDFSNCLYQDFRIPLSP
VHKCSFYKNNTKVSYGFLSPPQLNKNSSGIYSEALLTTNIVPMYQSFQVIWRYFHDTLLRKYAEER
NGVNVVSGPVFDFDYDGRCDSLENLRQKRRVIRNQEILIPTHFFIVLTSCKDTSQTPLHCENLDTLA
FILPHRTDNSESCVHGKHDSSWVEELLMLHRARITDVEHITGLSFYQQRKEPVSDILKLKTHLPTFS
QED.

FIGURE 67

GGTTTTCAAATGGAACATTTTGATGCATCACTTAGTACCTATTTCAAGGCATTGCTAGGCCCTC
GAGATACTAGAGTAAAAGGATGGTTTCTTCTGGACAATTATATACCCACATTTATCTGCTCTGT
CATATATTTACTAATTGTATGGCTGGGACCAAAATACATGAGGAATAAACAGCCATTCTCTTG
CCGGGGGATTTTAGTGGTGTATAACCTTGGACTCACACTGCTGTCTCTGTATATGTTCTGTGAG
TTAGTAACAGGAGTATGGGAAGGCAAATACAACTTCTTCTGTCAGGGCACACGCACCGCAGG
AGAATCAGATATGAAGATTATCCGTGTCCTCTGGTGGTACTACTTCTCCAAACTCATAGAATTT
ATGGACACTTTCTTCTTCATCCTGCGCAAGAACAACCACCAGATCACGGTCCTGCACGTCTAC
CACCATGCCTCGGTGCTGAACATCTGGTGGTTTGTGATGAACTGGGTCCCCTGCGGCCACTCTT
ATTTTGGTGCCACACTTAATAGCTTCATCCACGTCCTCATGTACTCTTACTATGGTTTGTCGTC
AGTCCCTTCCATGCGTCCATACCTCTGGTGGAAGAAGTACATCACTCAGGGGCAGCTGCTTCA
GTTTGTGCTGACAATCATCCAGACCAGCTGCGGGGTCATCTGGCCGTGCACATTCCCTCTTGGT
TGGTTGTATTTCCAGATTGGATACATGATTTCCCTGATTGCTCTCTTCACAAACTTCTACATTC
AGACCTACAACAAGAAAGGGGCCTCCCGAAGGAAAGACCACCTGAAGGACCACCAGAATGG
GTCCATGGCTGCTGTGAATGGACACACCAACAGCTTTTCACCCCTGGAAAACAATGTGAAGCC
AAGGAAGCTGCGGAAGGATTGAAGTCAAAGAATTGAAACCCTCCAAACCACGTCATCTGATT
GTAAGCACAATATGAGTTGTGCCCCAATGCTCGTTAACAGCTGCTGTAACTAGTCTGGCCTAC
AATAGTGTGATTCAAAGGGCGAATTCTTTCATCAATTCAAAACCCCTAGAAAACGTATACAGA
TTATATAAGTAGGGATAAGATTTCTAACATTTCTGGGCTCTCTGACCCCTGCGCTAGACTGTGG
AAAGGGAGTATTATTATAGTATACAACACTGCTGTTGCCTTATTAGTTATAACATGATAGGTG
CTGAATTGTGATTCACAATTTAAAAACACTGTAATCCAAACTTTTTTTTTTAACTGTAGATCAT
GCATGTGATTGTAAATGTAAATTTGTACAATGTTGTTATGGTAGAGAAACACACATGCCTTAA
AATTTAAAAAGCAGGGCCCAAAGCTTATTAGTTTAAATTAGGGTATGTTTCAAGTTTGTATTA
ATTTGTAATAGCTCTGTTTAGAAAAAATCAAAGACCATGATTTATGAAACTAATGTGACATAA
TTTCCAGTGACTTGTTGATGTGAAATCAGACACGGCACCTTCAGTTTTGTACTATTGGCTTTGA
ATCAAGCAGGCTCAAATCTAGTGGAACAGTCAGTTTAACTTTTTAACAGATCTTATTTTTTTAT
TTTGAGTGCCACTATTAATGTAAAAAGGGGGGGGCTCTACAGCAGTCGTGATGAAACTTAAAT
ATATATTCTTTGTCCTCGAGATTTTAGGAAGGGTGTAGGGTGAGTAGGCCATTTTTAATTTCTG
AAGTGCTAAGTGTTTTTATACAGCAAACAAAAAGTCAATTTTGCTTTCCACCAGTGCGAGAGA
GGATGTATACTTTTCAAGAGAGATGATTGCCTATTTACCGTTTGACAGAGTCCCGTAGATGAG
CAATGGGGAACTGGTTGCCAGGGTCTAAATTTGGATTGATTTATGCACTGTTATCTGTTTTGAC
ACAGATTTCCTTGTAAAATGTGCCTAGTTTACCAAAATTAACAAAGGGGGGGAAAGGACCTTA
GAACTTTTTAAGGTAAAATCAAATATAGCTACAGCATAAGAGAATCGAGAAATTTGATAGAG
GTAACTTGTTTAATGTAAATCTAATAGTACTTGTAATTTCTTTCTGCTTAGAATCTAAAGATGT
GTTTAGAACCTCTTGTTTAAAAATAATAGACTGCTTATCATAAAATCACATCTCACACATTTGA
GGCAGTGGTCAAACAGGTAAAGCCTATGATGTGTGTCATTTTAAAGTGTCGGAATTTAGCCTC
TGAATACCTTCTCCATTGGGGGAAAGATATTCTTGGAACCACTCATGACATATCTTAGAAGGT
CATTGACAATGTATAAACTAATTGTTGGTTTGATATTTATGTAAATATCAGTTTACCATGCTTT
AATTTTGCACATTCGTACTATAGGGAGCCTATTGGTTCTCTATTAGTCTTGTGGGTTTTCTGTTT
GAAAAGGAGTCATGGCATCTGTTTACATTTACCTTATCAAACCTAGAATGTGTATATTTATAA
ATGTATGTCTTCATTGCTAGGTACTAATTTGCAGATGTCTTTACATATTTCAATACAGAAACTA
TAACATTCAATAGTGTGCTGTCAAAGTGTGCTTAGCTCACCTGGATATACCTACATTGTTAAAT
GTCTAAACAGTAATCATTAAAACATTTTGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 6 8

MEHFDASLSTYFKALLGPRDTRVKGWFLLDNYIPTFICSVIYLLIVWLGPKYMRNKQPFSCRGILV
VYNLGLTLLSLYMFCELVTGVWEGKYNFFCQGTRTAGESDMKIIRVLWWYYFSKLIEFMDTFFFI
LRKNNHQITVLHVYHHASVLNIWWFVMNWVPCGHSYFGATLNSFIHVLMYSYYGLSSVPSMRPY
LWWKKYITQGQLLQFVLTIIQTSCGVIWPCTFPLGWLYFQIGYMISLIALFTNFYIQTYNKKGASRR
KDHLKDHQNGSMAAVNGHTNSFSPLENNVKPRKLRKD.

FIGURE 69

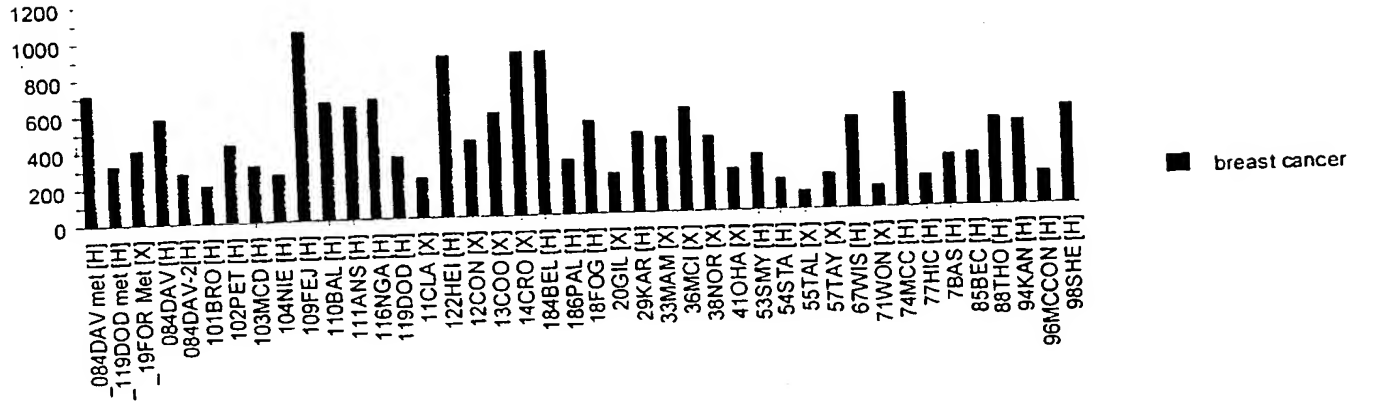


FIGURE 70

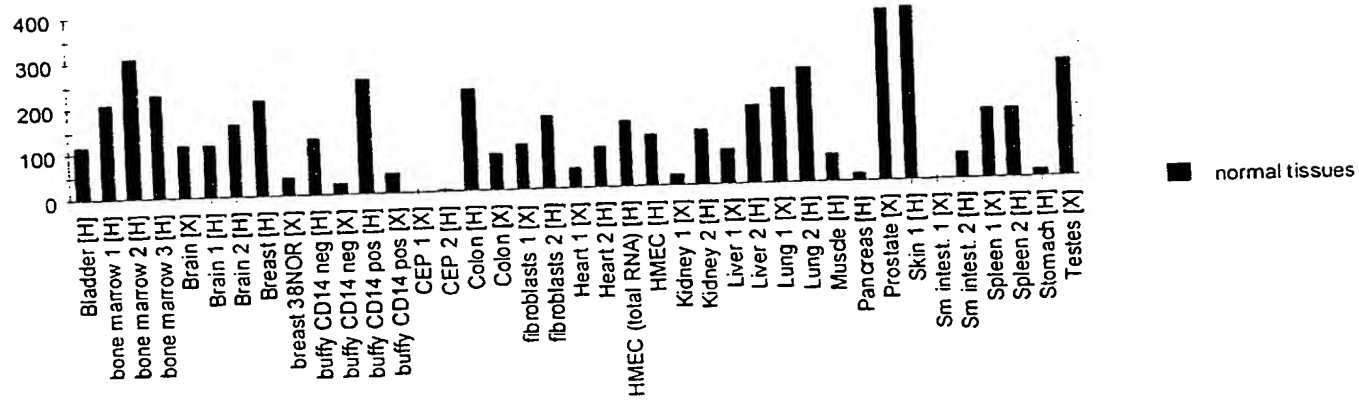


FIGURE 71

TTTTTTTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTTCATCCGTGAATGGTCCAGGGAAGGA
CCTTTCACCTTGACTATATGGCATTATGTCATCACAAGCTCTGAGGCTTCTCCTTTCCATCCTGCGTGGAC
AGCTAAGACCTCAGTTTTCAATAGCATCTAGAGCAGTGGGACTCAGCTGGGGTGATTTCGCCCCCCATCTC
CGGGGGAATGTCTGAAGACAATTTTGGTTACCTCAATGAGGGAGTGGAGGAGGATACAGTGCTACTACCAA
CTAGTGGATAAAGGCCAGGGATGCTGCTCAACCTCCTACCATGTACAGGGACGTCTCCCCATTACAACTAC
CCAATCCGAAGTGTCAACTGTGTCAGGACTAAGAAACCCTGGTTTTGAGTAGAAAAGGGCCTGGAAAGAGG
CGAGCCAACAAATCTGTCTGCTTCCTCACATTAGTCATTGGCAAATAAGCATTCTGTCTCTTTGGCTGCTG
CCTCAGCACAGAGAGCCAGAACTCTATCGGGCACCAGGATAACATCTCTCAGTGAACAGAGTTGACAAGGC
CTATGGGAAATGCCTGATGGGATTATCTTCAGCTTGTTGAGCTTCTAAGTTTCTTTCCCTTCATTCTACCC
TCCAAGCCAAGTTCTGTAAGAGAAATGCCTGAGTTCTAGCTCAGGTTTTCTTACTCTGAATTTAGATCTCC
AGACCCTTCCTGGCCACAATTCAAATTAAGGCAACAAACATATACCTTCCATGAAGCACACACAGACTTTT
CAAAGCAAGGACAATGACTGCTTGAATTGAGGCCTTGAGGAATGAAGCTTTGAAGGAAAAGAATACTTTGT
TTCCAGCCCCCTTCCCACACTCTTCATGTGTTAACCACTGCCTTCCTGGACCTTGGAGCCACGGTGACTGT
ATTACATGTTGTTATAGAAAACTGATTTTAGAGTTCTGATCGTTCAAGAGAATGATTAAATATACATTTCC
TACAAAAAAAAAAAAAAAAAAGTCGACG

FIGURE 12

AGAGATGGGGGTCTCACTATGTTGCCCAGGCTGGTCTCAAACTCCTGGGCTCAAGCGATCCTTTGGCCTCG
GCCTCCCAAAGTGCATGAGCCACCATGCCTGGCCTGTTTAGTTTTGTTTCAAGTTGAAATACCTTTCTTGT
GTTTTCTAATTAGAAAAGTAATATCTACTCATTGTAAAAACTCAAACAGTGCAGAAATGTAGAAAGTAGAA
AGTGTAAGTCCCTGGTTGTCCCTTCTGCCTGAGCACAACCACTGCTCACAGTTTGATGTATATCCTTCCAG
AGACTCTCAAATTTAAGCAAATAATTTTTATTACCATGTCTTTTTATTTGAAGACGTACATTTGCCTCCAA
AGTTCAACACAAGTTCAACTGACCATATCCTTCCATGACCTGAATAGATGCTATCCTTTATCACGATGTTC
AATTGCCTTTGAAAGAGAGTAGTCCAGGTATATTCCTGATCAAAATTTGGCATTTTTGATGATACTACTCT
ACACAGATCAGACTCATGTGCAGAATCGTGCCTGGAGAGAGAGGTTTGGTTAAGACAGAGATTTCTGGAAA
CATTCAAATTGCAAATGGAAACTTGAAACCCACAATCTAATGAGGAATGTACTGGAAAAATAATCTGAAGA
GTTGACAAATTGTGTACTAGATTGAACACATGGAATGCAATGCCAATGAGACTTTCTGCACTAAAACTTAT
CCTCATATGTACAACAATGATGTGTGTATTATATAACAGTGATGTGTACATTTCTGACACCCCATACATAA
TATACACAGTTTGTATAAATGCATACATTTAAAAATATATATGTACAATACAGCTAACATAAAACTGTAGT
ACGCCTGAAGGATATTACTAGTGCCTAATATTGAGTATGAGTCACTGCGTGTTCGCATCAACTTGGAAGTG
CAGTAATTGTTATAAAATTAATCAGTGCAGCCAACATTATTTATGAATCACATCTTTGAAACTGTGCAGTA
GCATATACATATATATTTTTAAATAACATTTTTCACAGTTTTCCAGAGTTACTGTTGAAATCTGCATCACC
AAAAAAAAAAAAAAAGCAAGATTTTTTTAACAATGTAGACACTCTTCAGACCCAGTAATCTGCGTGTGATTT
CCTATTTGTAGATTCCCAAGAGACTTTAGCAGTCACCAGCCTTAATGCATGTACAGGATATTATTGTGACT
TAATTTATCTGCAGTTTTTAATCCATGTGAAATTGGGAATTTTTAACCGAACTTGGATTAACCATGCCTGC
CTTTCTAAGGTTGCAAATGTTACATTAAATGATTTATGTTGTAAAAAAAAAAAA

FIGURE 13

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09/440,676	16 November 1999 (16.11.1999)	US
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09/450,810	29 November 1999 (29.11.1999)	US
09/453,137	2 December 1999 (02.12.1999)	US
Not furnished	8 March 2000 (08.03.2000)	US

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(72) Inventors; and

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(74) Agents: SILVA, Robin, M. et al.; Flehr Hohbach Test Albritton & Herbert LLP, Suite 3400, 4 Embarcadero Center, San Francisco, CA 94111-4187 (US).

(81) Designated States *(national)*: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

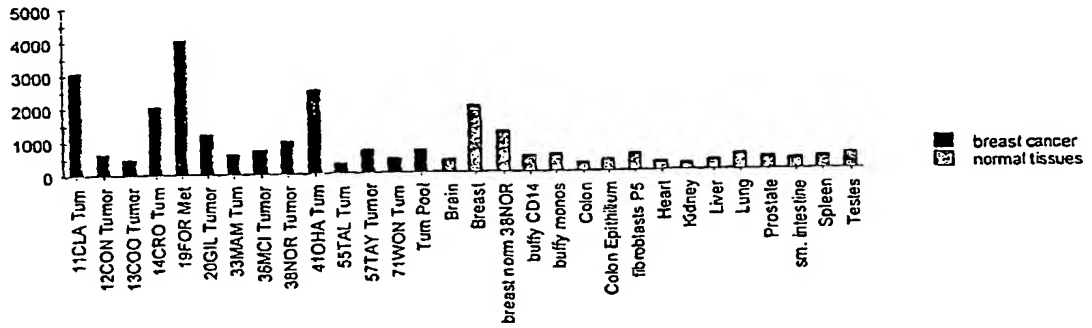
— *With international search report.*

— *Before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments.*

(88) Date of publication of the international search report:
22 March 2001

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSING AND TREATING BREAST CANCER



(57) Abstract: Described herein are methods that can be used for diagnosis and prognosis of breast cancer. Also described herein are methods that can be used to screen candidate bioactive agents for the ability to modulate breast cancer. Additionally, methods and molecular targets (genes and their products) for therapeutic intervention in breast and other cancers are described. The methods involve the use of proteins like BCH1.

WO 00/55629 A3

INTERNATIONAL SEARCH REPORT

Interr nal Application No
PCT/US 00/06952

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 G01N33/574 G01N33/50

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal, WPI Data, PAJ, STRAND, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 18945 A (ABBOTT LAB) 7 May 1998 (1998-05-07) claims 17,20; examples 3,19 page 49, line 1 - line 8 page 33, line 3 -page 38, line 2	1-32, 35-37
A	WO 98 34118 A (UNIV YALE) 6 August 1998 (1998-08-06) claims 1,29	1-37
A	US 5 514 554 A (BACUS SARAH S) 7 May 1996 (1996-05-07) claim 1	1-37
P,X	WO 99 23230 A (ABBOTT LAB) 14 May 1999 (1999-05-14) abstract	9

-/--

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

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"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
28 November 2000	- 5. 12. 00

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Gundlach, B

4

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INTERNATIONAL SEARCH REPORT

Intern nal Application No
PCT/US 00/06952

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category ˇ	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO 99 33869 A (CORIXA CORP) 8 July 1999 (1999-07-08) abstract	9
P,X	WO 00 08210 A (RECIPON HERVE ;DIADEXUS LLC (US); SUN YONGMING (US); CAFFERKEY ROB) 17 February 2000 (2000-02-17) the whole document	9
P,X	WO 99 25877 A (ABBOTT LAB) 27 May 1999 (1999-05-27) page 32, line 32 -page 36, line 9	1-3,6,7, 15

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

In. ational application No.
PCT/US 00/06952

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.: –
because they relate to subject matter not required to be searched by this Authority, namely:

see FURTHER INFORMATION sheet PCT/ISA/210

2. [ ] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [X] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

1-3,6,7,15 (partially, in so far as they relate to inventions 1 and 3),
4,5,8-14,16-37 (fully)

4. [ ] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[X] No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.1

Although claims 6,7 are directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
Although claims 28,31-34 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

Continuation of Box I.1

Rule 39.1(iv) PCT - Diagnostic method practised on the human or animal body and/or method for treatment of the human or animal body by therapy

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-3,6,7,15 (partially) 4,5,8-14,16-37 (fully)

   Method of screening drug candidates involving BCH1

2. Claims: 1-3,6,7,15 (partially)

   Method of screening drug candidates involving BCA2

3. Claims: 1-3,6,7,15 (partially)

   Method of screening drug candidates involving BCJ7

4. Claims: 1-3,6,7,15 (partially)

   Method of screening drug candidates involving BCN1

5. Claims: 1-3,6,7,15 (partially)

   Method of screening drug candidates involving BCN5

6. Claims: 1-3,6,7,15 (partially)

   Method of screening drug candidates involving BCO2

7. Claims: 1-3,6,7,15 (partially)

   Method of screening drug candidates involving BCQ5

8. Claims: 1-3,6,7,15 (partially)

   Method of screening drug candidates involving BCR2

9. Claims: 1-3,6,7,15 (partially)

   Method of screening drug candidates involving BCX2

10. Claims: 1-3,6,7,15 (partially)

    Method of screening drug candidates involving BCY3

INTERNATIONAL SEARCH REPORT

...ormation on patent family members

Intern ...al Application No
PCT/US 00/06952

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9818945 A	07-05-1998	EP 0939824 A	08-09-1999
WO 9834118 A	06-08-1998	AU 6051298 A	25-08-1998
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		EP 1042360 A	11-10-2000
		ZA 9811800 A	23-06-1999
WO 0008210 A	17-02-2000	NONE	
WO 9925877 A	27-05-1999	EP 1032706 A	06-09-2000